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957 GGGAGAAGGTGACGCTCTGCATCTCCGTGCTCCTCTCCCTGACGGTCTTTCTCCTCGTGA 1016
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                                                                                                                                                                                                                                                                                                                                                                   240 CCTCGGAAGCTGAGCACCGCCTGTTCCAGTACCTGTTTGAAGATTACAACGAGATCATCC
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                                                                                                                                               TGGCGGCGCCCGCGGGGCCTGCTGCTGCTGTGCCTGCTCTGGCCCGAGGGGGGGCACGCT
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       DB 11; Length 3126;
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Score 281.6; DB 11;
Pred. No. 7e-44;
0; Mismatches 469;
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55.0%;
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                                                                                                                                                                                                                                                                                                                                            Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiraoka, T., Hirozane, T., Hori, F., Imocani, K., Ishia, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Itoh, M., Kogawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nakai, K., Numazaki, R., Ohno, M., Ohazaki, Y., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sakazume, N., Sagabe, Y., Tagawa, R., Takakashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomau, A., Toya, T., Yasunishi, A., Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enriched mouse cDNA library
                                                                                                                                                                                                                       on functional annotation
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                                                                                                                                               Exploration Research
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                                  Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                                                                               Genome
                                                                                                                                                                             Group Phase I & II Team.
Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3126)
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/clone="A730007P14"
/issue type="cerebellum"
/clone_lib="RIKEN full-length
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                                                                                                                                               Consortium and the RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon start=1
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JOURNAL
                                                                    JOURNAL
                                                                                                             REFERENCE
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                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
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688 836 748

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Dp.

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/codon start=1
/protein id="BAC26337.1"
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HT anslation="MELSTVLILLGLGSAGLVLGSEHETRLVAKLFEDYSSVVRPVED HREIVQYVTGGLLGLINDEVNG1VTTNVRLKQQWVDYNLKWNPDDYGGVKKTHIPS EKIWRPDVVLYNNADGDFAIVKFTKVLLDYTGHITWTPPAIFKSYCEIIVTHFPFDEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKEARGWKHWVFYSCCPTTPY
LDITYHFWWRLPLPYFIVNVIIPCLLFSFLTSLVFYLPTOSTGERWTLSISVLLSTTVF
LLVIVELIPSTSSAVPLIGKYMLFTWYVVIASIITTVIVINTHRSPSTHNMPEWRK
VFIOTIPNIMFFSTWKRPSRDKQEKRIFTEDIDISDISGKPOPPPMGFHSPLIKHPEN
KSAIEGVKYIAETMKSDQESNNAAEEWKYVAMVMDHILLGVFMLVCLIGTLAVFAGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                      Research Group in Riken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 GAAAAAATTCACATCCCCTCGGAAAAGATCTGGCGGCCGGACGTCGTTCTCTATAACAA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="unnamed protein product; cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) (MGD|MGI:87885, GB|NM_007389, evidence: BLASTN, 99%, match=1763)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 ACAGCIGAICCAGCITAICAAIGIGGAIGAAGIAAAICAGAIIGIGACAACCAAIGIACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 GCGCCGCTCGCACTTGGCGGCGCCCGGGGCCTGCTGCTGCTGCTGCTGCTCTTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 écégciacical de la contra del la contra dela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 redecriferreregécrecgaacardagaedecereregregeaaagererrirgaagaera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 CAACGTACTGGAGAGGCCCGTCGTCAACGAGGGGACCCGCTGCAGCTCTCCTTCGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 CAGCAGTGTAGTCCGGCCAGTGGAGGACCACCGTGAGATTGTACAAGTCACCGTGGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 GCTAAAACTAGAGTGGAATGATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 TCTGAAACAGCAATGGGTCGATTACAACTTGAAATGGAATCCAGATGACTATGGAGGAGT
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.8%; Score 280.4; DB 11; Length 4290; 54.5%; Pred. No. 1.3e-43; ive 0; Mismatches 465; Indels 0;
                                                                                                                                                                                                                                                                                                                 prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
mol_type="mRNN"
/strain="C57BL/6J"
/db_xref="MG1.2391228"
/db_xref="MG1.2391228"
/db_xref="MG1.2391228"
/db_xref="HG1.2000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="0 day neonate"
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Analysis of the mouse transcriptome based on functional annotation of 60 for full-length cDNAs

Inature 420, 563-573 (2002)

E (Dasses 1 to 4290)

E (Dasses)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, W., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kodno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Okazaki, Y., Salto, R., Nomura, K., Numuzaki, R., Ohno, M., Okazaki, Y., Salto, R., Saltoh, H., Sakai, C., Sakai, K., Sakazume, N., Sagabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Haraka, Y., Tanaka, T., Towar, S., Takahashi, F., Takaka, T., Takahashi, R., Tayaka, T., Yasunishi, A., Haraka, S., Andanaka, M., Andanaka, M., Tagawai, Y., Tayaki, Y., Tayaka, Y.,
                                                                                                                                                                                                                               AKU29177

Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched alpha polypeptide 1 (muscle), full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA cloning
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                      Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 278.4; DB 29;
Pred. No. 2.2e-43;
); Mismatches 436;

    1374
    organism="Mus musculus"

                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:10090"
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/gene="CHRNA1"
/locus_tag="HCM2488"
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                               CCCCTTCGACGACGACGATGCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCA
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
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I (bases, 1 to 1466)
Jin, P., Feu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R., Au-Young, J. and Stuve, L.L.
                                                                                                         CAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGTGCGTCTGAAACAGCAATGGGT
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                                                    CGACGTGGACGAGAAGAACCAGCTTTTAATAACAAACATCTGGCTAAAACTAGAGTGGAA
                                                                                                                                                                   TGATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAGTGCC
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Homo sapiens CHRNAl gene, VIRTUAL TRANSCRIPT, partial sequence,
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                        CATCATGTTCATGGTGGCTTCCTCCGTCTCCACCATACTGATCCTCAACTACCACCA
                                                                                                                                                                                                                                                                                                             GGAGCCTGGCCTCTCCTGCTCTTTTAGCCTTTTGCTCAGCTGGCCTCGTCCTGGGCTC
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                                                                                                                                            GGCGGGGGCGACGACGTCGGACGCCGTGCCTTGCTCGGCACCTACTTCAACTG
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 9
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                                                                                                                                                                                                                                                                                                                                                                       CCGGCACGCAGACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTT 1037
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/organism≃"Homo sapiens"
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/db_xref="taxon:9606"
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/locus_tag="HCM2488"
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56.0%;
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Catarrhini; Hominidae; Homo.
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
                                                                                       750 GCCCTGCGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCCAGACTCCGG
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Homo sapiens CHRNA3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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1 (Dases 1 to 1456).
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Trodd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Pred. No. 5e-42;
0; Mismatches 431;
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.larity 56.1%; Pred. No. 1.4e-42;
Conservative 0; Mismatches 433; Indels 6;
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                                                                                                                                                                                                   CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
PCR isolation and cloning of now drug target genes drugulished (2003) Contact: Jin, P. Incyte Corporation 3160 Porter Drive, Palo Alto, C? Tel: 650 621 8639 Fax: 650 621 8965 Email: plin@incyte.com.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 1436)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
First sequence was made by sequencing genomic exons and ordering them based on alignment.
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Pred. No. 1.1e-41;
                                                                                                                                                                                                                                                                                                                                                                                         Science 302 (5652), 1960-1963 (2003)
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Pan troglodytes CHRNA3 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                        21 CTCGCACTTGGCGCCCCGCCGGGCCTGCTGCTGCTGCTGTGCTCTTGCTCTGCTCTGGCCGAGGGG
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
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0
                                                                                                                                                                                                      607;
                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                  0; Mismatches 171;
                                                                                                                                                                                                      Score 269.4; DB 9;
Pred. No. 8.8e-42;
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AI292581

MRNA linear EST 02-DEC-2003

ABHIS518.5prime GH Drosophila melanogaster head p072 Drosophila
melanogaster CDNA clone GH15518 5 similar to CG4128: Fban0004128

'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence.
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea; Drosophilidae, Drosophila.
1 (Dases 1 to 607)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
                        TCTGATCGTGCCTGCGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCC
                                                                                                                                                                                                                                                                                                                             719 caacigradadadadadacereracarerecarecrecerereceraacagrerirer
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Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE00326: arm:2L [9617316,9882551]
hit genomic AE00326: arm:0L [9617316,9882551]
estimated-cyto:30C7-30F4: 04/10/2001
Plate: GH.155 row: B column: 6
High quality sequence stop: 521
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/lab_host="DH5 - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Drosophila melanogaster
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/db_xref="taxon:7227"
/clone="GH15518"
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857 999

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AK080475

2010 bp mRNA linear HTC 19-SEP-2003
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:A730038F14 product:NBURONAL NICOTINIC
AKCEYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
AK080475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komo,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                        1000 GACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCTTTATTGGCTGCCGTGGGTG 1059
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Nature 420, 563-573 (2002)
6 (bases 1 to 2010)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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rodd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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    1436
    /organism="Pan troglodytes"
    /mol_type="genomic DNA"
    /db_xref="taxon:9598"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="CHRNA3"
/locus_tag="HCM1369"
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Arangawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Muraca, M., Makamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sasaki, Y., Saito, R., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A., Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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/db_xref="MGI:2408016"
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ORIGIN

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 11:09:28 ; Search time 42.6667 Seconds (without alignments) 3284.615 Million cell updates/sec May on: Run

1 MGGRARRSHLAAPAGLILLL.....LFTIIATLAVLLSAPHIMVS 496 US-09-303-232-4 2665 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* geneseqp1980s:* geneseqp1990s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aav50815 H. viresc	<u></u>	Ξ.	Dro			m	Aaw09025 Neuronal	Aab24088 Human PRO		Aab50012 Wild-type	Abq70492 Human neu	5 Human	Adal0874 Human neu	Human	Ade57310 Human Pro	Aaw69216 V274T var	Aab50015 Mutant hu	Aab50016 Mutant hu	Ade57308 Rat Prote	Rat	Muta	Aaw12369 Neuronal		_
SUMMARIES	DI OI	AAY50815	AAY50814	AAY50816	ABB63683	AAW12368	ABB60432	AAW44153	AAW09025	AAB24088	AAB82690	AAB50012	ABG70492	ABB82435	ADA10874	ADD47051	ADE57310	AAW69216	AAB50015	AAB50016	ADE57308	ADD47049	AAB50017	AAW12369	AAE12824	ABP96318
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AAB50014	AAB50018	ABB60716	AA017243	ADE57314	ADE57318	AAW09022	ADA10857	AAW44155	AAR73966	AAW09021	ABG61850	ABG31800	ABB82430	ADA10855	ADC71171	ADC71169	ADD45584	ADE59169	ADA83810
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26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR. H. virescens acetyl-choline receptor protein from clone Hva7-1. AAY50815 standard; protein; 496 AA. 17-FEB-2000 (first entry) Heliothis virescens DE19819829-A1 11-NOV-1999 AAY50815; RESULT 1 AAY50815

98DE-01019829 04-MAY-1998;

98DE-01019829 04-MAY-1998;

(FARB) BAYER AG.

Schulte T; Adamczewski M, Oellers N,

WPI; 2000-014207/02. N-PSDB; AAZ24476.

New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.

Example 1a; Page 17-19; 26pp; German

This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens

Sequence 496 AA;

insects, used to identify potential insecticides.

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Length 496;
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 5; DB 3;
4.5e-257;
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0; Mismatches
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 Query Match 100.
Best Local Similarity 100.
Matches 496; Conservative
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere which neurotransmission. (1) (also vectors containing it, its regulatory regions, and antibodies directed against (1)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved information of functionally related ACHR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an accetyl-choline receptor isolated from Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               615 DISSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acetyl-choline receptor protein from clone Hva7-2.
                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                           Length 770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   535 SMALLGPTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-
                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  461 KFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIMVS 496
                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                             69.4%; Score 1850; DB 3; 70.0%; Pred. No. 2.4e-175;
                                                                                                                                                                                                                                                                                                                             30; Mismatches
                                Example la; Page 12-14; 26pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                              Similarity 70.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heliothis virescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGEENGAG-
                                                                                                                                                                                                                                                                 Sequence 770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H. virescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-FEB-2000
                                                                                                                                                                                                                                                                                                                                 361;
                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137
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Sequence 311
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476
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                                                                  ABB63683
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                            This invention describes a novel nucleic acid (NA) encoding a nicotinic acety-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere with neurotransmission. (1) (also vectors containing it, its regulatory regions, and antibodies directed against (1)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AchR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (1) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CVLISSMALLGFTLFPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEGGGDISSEVINGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPPARV- 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----EENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRL 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIYPINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APAGLILLICLIMPRGARCGYHEKRILHHILDHYNVLERPVVNESDPLQLSFGLTLMQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPPPDLEIRERSSKSLLANVLDIDDDFRH----PQAQQ-----PQCCRY---YRGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRMRELELKERSSKSLLANVLDIDDDFRHGPPPNSTASTGNLGPGCSIFRTDFRRSFVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                              New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1803.5; DB 3; Pred. No. 5.8e-171; 53; Mismatches 78;
                                                                                                                                              Schulte T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLIFTLFTHATLAVLLSAPHIMV 495
                                                                                                                                                                                                                                                     Example la; Page 22-23; 26pp; German.
                                                              98DE-01019829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.7%;
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Best Local Similarity 68.7°
Matches 347; Conservative
                                                                                                                                                                       2000-014207/02.
                                                                                                                                                                      WPI; 2000-014207/
N-PSDB; AAZ24477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 501 AA;
                                                                                                                                            Adamczewski M,
                                                                                                                (FARB ) BAYER
        DE19819829-A1
                                                              04-MAY-1998;
                                  11-NOV-1999
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGRARRSHLAAPAGLLLLCLLWPRGARCGYHEKRLLHHILLDHYNVLERPVVNESDPLQL
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                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.2%; Score 1417.5; DB 4; Length 311; 87.2%; Pred. No. 1.1e-132; ive 14; Mismatches 16; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 17841; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 17841.
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CLFVFTLFTIIATVAVLLSAPHIIV 500
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                                                                                                                                                                 protein; 311
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75.
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ses 265; Conserv
                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
53 VYFILSLMQIMDVDEKNQVLITINIMLQMYWTDHYLQWNVSEYPGVKNVRFPDGLIMKPDI
                                                                        E----DKVRPACQHKQRRCSLSSMEMNTVSGQQCSNGNMLYIGFRGLDGVHCTPTTDS
                                                                                                                                                                                                                                                                                                                                                                                                                                       GVICGRMTCSPTEEBILLHSGHPSEG-DPDLAKILEEVRYIANRFRDQDEEEAICNEWKF
                                                       LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT
                                                                                                                           YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK
                                                                                                                                                                                                 TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA
                                                                                                                                                                                                                                                                        VPLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG
                                                                                                                                                                                                                                                                                                                                                                                                                  405 PQCCRYYRGG--BENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 8088; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                           SATTPPPARVPPPDLELRERSSKSLLANVLD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 8088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PWD,
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11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The alphal subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid sequences of chick neuronal alpha-bungarctoxin binding protein (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97) obtd. from an 18-day chick embryo CDNA library. ABBP subunits can be produced in recombinant host cells, pref. a bacterium, and used in the screening of cholinersic agents and other drugs that may affect the ligand binding, ion channel or other activity of intact ABBP subtypes. The ABBP alphal as immunogens for preparing antibodies to produce subunit peptides for use subtypes and their histological location
                          61 LSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV 120
       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52
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       LYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGGRARRSHLAAPAGLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated neuronal alpha-bungaro-toxin-binding protein DNA - used screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                             Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                            Neuronal alpha-bungarotoxin binding protein alphal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.5%; Score 1267; DB 2;
48.6%; Pred. No. 2.5e-117;
ive 83; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23. .502
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Sig_peptide
                                                                                                                                                                                                       standard; protein; 502 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89US-00413947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schoepfer RD;
                                                                                                                                                                                                                                                                                                                                                                  ligand binding; ion channel
                                                                                                                                                                                                                                                                          (first entry)
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1es 249; Conservative
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                                                                            PLLG 305
                                                                                                              PLLG 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lindstrom JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-1989;
                                                                                                                                                                                                                                                                          17-JUN-1997
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                                                                                                                                                                                                     AAW12368
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Protein Peptide

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TILLSLTVFLNMVAETMP-----ATSDAVPLLGTYFNCIM 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RNEIYYNCCPEPYIDI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ILFFQFN----CAMCANLIDGPTGLHIAAGFGRETDAGRNYTTIINSISKP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FMVASSVVSTILILLNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP- 371
                                                                                                                                                                                                                                                                                                                                                                        8 SHLAAPPAGLILILICLIMPRGARC-GYHEKRLLHHILDHYNVLERPVVNESDPLQLSFGLT 66
                                                                                                                                                                                                                                                                                                                                                                                                      insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL1675) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 TFAVVIRRKTLYYFFNLIVPCVLIASM-----ALIGFTLPPDSGEKLSLGV----
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                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102;
                                                                                                                                                                                                                                                         47.0%; Score 1253; DB 4; Length 498; 50.4%; Pred. No. 6.1e-116; Live 53; Mismatches 108; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "transmembrane domain"
262. .284
/label= TMD2
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/label= signal
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/label= TMD1
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Best Local Similarity
Matches 267; Conserv
                                                                                                                                                                                                       Sequence 498 AA;
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The present sequence represents a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta NAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits on specific receptor subunit combinations with a variety of potential agonists or anteagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells that express a variety of subtypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131
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y of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 APAGLILLICLIWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 ATFHTNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human neuronal nicotinic acetylcholine receptor subunits and DNA - al
transformed cells useful for screening cpds. which modulate activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.8%; Score 1246; DB 2;
46.0%; Pred. No. 3.1e-115;
iive 86; Mismatches 126;
              290. 317
/label= TMD3
/note= "transmembrane domain"
'note= "transmembrane domain"
                                                                                                                                                                 /note= "transmembrane domain"
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                                                                                /label= cytoplasmic_loop
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                                                                                                                'note= "encoded
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                                                                                                                                 462. .487
/label= TMD4
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                                                                                                                                                                                                                                                                                                     93US-00028031
                                                               .461
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Best Local Similarity 46.0<sup>3</sup>
Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-303024/37.
                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV12197
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                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                   08-MAR-1994;
                                                                                                                                                                                                                                    15-SEP-1994
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71 63 123 191 183 251 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300

CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311

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STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191
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                                                                                                          DEGGGDISSFVTNGEWELIGVPCKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                                                                                                                                                                   CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI
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                                                                                                                                                                                                                                                                                                                                                                                    --SATTPPPAR---
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99WO-US012252.
99US-0141037P.
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99WO-US030911
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N-PSDB; AAC58395.
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02-JUN-1999;
23-JUN-1999;
07-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The alpha-7 subunit (AAW09025) of the human neuronal nicotinic actylcholine receptor (nAChR) can be expressed in transformed host cells carrying alpha-7 subunit DNA (see also AAV48239). Host cells, esp. mammalian cells or amphibian occytes, expressing the recombinant alpha-7 subunit, opt. in combination with other recombinant alpha and/or beta subunit, opt. in combination with other recombinant alpha and/or beta subunits (see also AAW09018-24) AAW09026-27), can be used to examine the function of human AChR and to identify cpds. that modulate its activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding nicotinic acetyl:choline receptor sub-units - used in screening to determine the effect of drugs on the receptor.
                                          MIIVGLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHK 360
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                                                                                         --VPPPPDLELRERSSKSLLANVLD
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                                                                                                                                   QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
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MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG---
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                                                                                                                                                                                                                                                                                               46.8%; Score 1246; DB 2;
46.0%; Pred. No. 3.1e-115;
live 86; Mismatches 126;
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                                                                                         --SATTPPPAR--
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English.

The propreparation of cancer. The antibodies and other anti-tumour compounds maybe used to treat various conditions, including those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, heaptic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, stromal and blastococelic disorders, and inflammatory, angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR primers and immunologic disorders used in the isolation of the human PRO sequences. AAC5836 and AAE34039 represent human PRO polymucleotide and protein sequences given in the exemplification of the The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619, PRO117, PRO809, PRO8030, PRO8030, PRO8030, PRO8030, PRO1005, PRO1005, PRO1005, PRO1005, PRO1005, PRO1005, PRO1005, PRO1005, PRO1005, PRO1181, PRO31, PRO311, PRO311, PRO1110, PRO21094, PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer. Claim 61; Fig 58; 286pp; present invention

Sequence 502 AA;

9 360 DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP 251 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLVABIMPATSDSVPLIAQYFAST 300 -VPPPPDLELRERSSKSLLANVLD 392 393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE 452 DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131 STYPTNVVVRNNGSCLYVPPGLFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191 CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311 12 APAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII 71 SPGGVWLALAASLIHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM 63 361 QRRCSLASVEMSÄVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----Gaps 70; Length 502; MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-46.8%; Score 1246; DB 3; Length 5 46.0%; Pred. No. 3.1e-115; ive 86; Mismatches 126; Indels SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494 153 DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494 ---SATTPPPAR---240; Conservative Similarity -DEHLLH-72 124 132 192 184 312 Query Match 252 361 Local Matches g 셤 g 8 셤 ò q δ ð g õ Q à δ g ò ð

Nicotinic acetylcholine receptor; nAChR; human; acetylcholine binding protein; AChBP; mollusc; ligand-binding protein; ligand-gated ion channel; crystal; drug design; protein co-ordinate data; schizophrenia; Alzheimer's disease; nicotine addiction; Tourette's syndrome; therapy; nootropic; neuroprotective. 108. .115 /note= "conserved ligand-binding region, residues Trp108 and Tyril5 are essential" residues Tyr210, /note= "conserved ligand-binding region, residues Trpl71 and Tyrl73 are essential" Water-soluble ligand-binding proteins derived from molluscs and analogs of ligand-gated ion channels, useful in drug screening assay, where the drugs identified can be used in the treatment of Alzheimer's disease or /note= "conserved ligand-binding region, Cys212, Cys213 and Tyr217 are essential" Nicotinic acetylcholine receptor alpha7. (TEWE-) STICHTING TECH WETENSCHAPPEN. Location/Qualifiers AAB82690 standard; protein; 502 09-FEB-2001; 2001WO-EP001457. 10-FEB-2000; 2000EP-00200443. 31-OCT-2000; 2000EP-00203810. (first entry) .217 210. WPI; 2001-497071/54. WO200158951-A2 sapiens 15-OCT-2001 16-AUG-2001 AAB82690; Smit AB, Region Region Region Homo Key AAB82690

schizophrenia.

Disclosure; Page 252-254; 260pp; English.

The present sequence is that of the alpha subunit of human nicotinic acetylcholine receptor (nAchR). The sequence includes regions that are conserved throughout the various nAchR alpha subunits and which are essential for ligand binding. The invention relates to water-soluble ligand-binding proteins derived from molluscs, especially acetylcholine-binding proteins (AchBERs) and analogues of ligand-gated ion channels, their crystals, and their use for screening ligand-ogated ion channels, their crystals, and their use for screening ligand-ogated ion channels. The water-soluble ligand-binding proteins are capable of channels. The water amenable to crystallization. The crystal structure of AChBP is provided, and can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated ion channels and the structure of AChBP is provided that are capable of binding a ligand of a ligand-gated receptor, and comprise at least the amino acids of the AchBP determining solubility of the AChBP, in the same positions as in the achieving solubility of the AChBP, in the same positions as in the chineric proteins, at least the amino acids of at least to the conserved regions of an nAChR have been substituted for the conserved regions of an nAChR have been substituted and argae and preferably entire stretches have been substituted. New drugs can be developed that selectively intervene in neuronal signalling pathways, especially where the ligand-gated ion channel is the nAChR, and the related disorder is Tourette's syndrome,

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-DEHLLH-
N-PSDB; AAC90380
                                                                                                                            Sequence 502 AA;
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                                                                                                                                                                                                              MIIVGLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHK 360
                                                                  71
                                                                                  63
                                                                                                             -----DPDLAKILEEVRYIANRFRCQDE
                                                                                 SPGGVMLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM
                                                                                                   DVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
                                                                                                                                   STYPINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                                                                                     CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI
                                                                                                                                                                                                                                                                      ---VPPPPDLELRERSSKSLLANVLD
                                                                                                                                                                                                                                                                                     QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                                                                                                                                       IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                  12 APAGLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII
                                                                                                                                                                    DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                  Gaps
                                                  70;
nicotine or schizophrenia
                                                                                                                                                                                                                                      MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; alpha7 nicotinic acetylcholine gated ion channel; 5-hydroxytryptamine; 5-HT3; calcium ion conductance.
                                 Length
                                                                                                                                                                                                                                                                                                                                                SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                       DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                Score 1246; DB 4;
Pred. No. 3.1e-115;
5; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wild-type human alpha7 ligand gated ion channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berkenpas MB
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addiction to
                                                                                                                                                                                                                                                                      ----SATTPPPAR----
                                                  98;
                                                                                                                                                                                                                                                                                                                                                                                                 AAB50012 standard; protein; 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PHAA ) PHARMACIA & UPJOHN CO
                                46.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-2000; 2000WO-US011862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0136174P
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wolfe ML,
Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-061524/07.
                                          Similarity
                                                                                                                                                                                                                                                                                                                       -DEHLLH
                 502 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200073431-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-DEC-2000.
                                                   Matches 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Groppi VE,
                                                                                                                                                   124
                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                      393
                                                                                                                                                                                                                                                                                                                                                                                                                 AAB50012;
                 Sequence
                                                                                                   72
                                                                                                                                   132
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                                 Query Match
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                                           Local
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Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
                                                                                                                                                       The present sequence is wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 APAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIYPTNIVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --VPPPPDLELRERSSKSLLANVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATHINVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 SPGGVWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVDEKNOLLI TNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEGGGDISSFVINGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRKTLYYFFNLIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nicotinic acetylcholine receptor; nNAChR; receptor; 9 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human neuronal nicotinic acetylcholine receptor alpha 7 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                   70;
                                                                                                                                                                                                                                                                                                                                                                                                 Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                               46.8%; Score 1246; DB 4; I
46.0%; Pred. No. 3.1e-115;
ive 86; Mismatches 126;
                                                                                                           Disclosure; Page 61-63; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 46.0
Matches 240; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----VPPPPDLELRERSSKSLLANVLD 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DPDLAKILEEVRYIANRFRCODE 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 APAGLILLICLIMPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                            Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.8%; Score 1246; DB 5;
46.0%; Pred. No. 3.1e-115;
iive 86; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 101; Col 59-64; 56pp; English.
                                                                                                                                                                                                 Harpold MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SATTPPPAR--
                                                                                        90US-00504455.
92US-00938154.
93US-00028031.
                                                             95US-00487596
                                                                                                                                      93US-00149503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                   Ellis SB,
                                                                                                                                                                    CO INC
                                                                                                                                                                                                                                WPI; 2002-711528/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
ses 240; Conserv
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                                                                                                                                                                      بي
                                                                                                                                                                                                                                                N-PSDB; ABS54875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 502 AA;
                                                                                                                                                                   (MERI ) MERCK
                                                                                                                                                                                                 Elliott KJ,
US6440681-B1
                                                           07-JUN-1995;
                                                                                                       30-NOV-1992;
08-MAR-1993;
                                                                                                                                      18-NOV-1993;
                              27-AUG-2002
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Cell comprising nucleic acids encoding human alpha and beta subunits of neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nuclectides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NAChR). The compositions and methods of the present invention, which provide a means to prepare synthetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NAChR alpha? subunit
                                                                                                                                                                                                                                                     nicotinic acetylcholine receptor; NAChR; drug screening; NAChR alpha7 subunit; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 APAGLILILICLIMPRGARCGYHEKRILLHHILDHYNVLERPVVNESDPLQLSFGLTLMQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elliott KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ъ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Siegel
                 SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGIIMSAPNFV
453 DADISRDWKFAAMVVDRLCLIFTLFTIIATLAVLLSAPHIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.8%; Score 1246; DB 5;
46.0%; Pred. No. 3.1e-115;
iive 86; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chavez-Noriega LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 130-131; 143pp; English.
                                                                                                                                                                                                                   Human neuronal NAChR alpha7 subunit.
                                                                                                                 ABB82435 standard; protein; 502
                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-2001; 2001WO-US050985.
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2000; 2000US-00703951
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 46.09
Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gillespie A, Claeps BO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-698532/75.
N-PSDB; ABV73248.
                                                                                                                                                                                                                                                                     immunochemistry;
                                                                                                                                                                                                                                                         neuronal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 AA;
                                                                                                                                                                                                                                                                                                                                         WO200259266-A2
                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                   22-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                            01-AUG-2002
                                                                                                                                                   ABB82435;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding an alpha-6 or a beta-3 subunit of a human neuronal nicotinic acetylcholine receptor (nAChR), useful for identifying compounds that modulate human neuronal nAChR activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human neuronal nicotinic acetylcholine receptor nAChR. nAChR's form ligandgated ion channels that mediate synaptic transmissions between nerve and wuscle and between neurons upon interaction with the neurotransmitter acetylcholine. The nucleic acid molecule is useful for identifying compounds that modulate human neuronal nAChR. The present sequence acetylcholine receptor, nAChR, alpha 7 subunit #1. Note: the present sequence encoded by the nAChR alpha 7 subunit DNA ADA10864.
  251
                                                      DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRKTLYYFFNLIVP
                                           CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTVFNCI
                                                                                                                                  --VPPPPDLELRERSSKSLLANVLD
                                                                                                                                                                             393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                      MFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG------
                                                                                                                                                       361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                                                                                                                                                                                                                   Human neuronal nicotinic acetylcholine receptor alpha 7 subunit #1
                                                                                                                                                                                                                                                                                                                                                                                     alpha 7 subunit; human; neuronal nicotinic acetylcholine receptor; ligand-gated ion channel; synaptic transmission; gene therapy; transgenic; receptor.
                                                                                                                                                                                                                                   SEAVCSEWKPAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                       DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 67-72; 63pp; English.
                                                                                                                                                                                                                                                                                                  ADA10874 standard; protein; 502 AA
                                                                                                                                  --SATTPPPAR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elliott KJ, Harpold MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MERI ) MERCK & CO INC
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                                                                                                                                                                                                  -DEHILH
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                                                                                                                                                                                        DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP 251
                                                                                                                                                                                                                                                                                                                                                                                 CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311
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                                                                                                                                                                        DVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
                                                                                                                       4 SPGGVWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM
                                                                                                                                                                                                                                                               12 APAGLILLICLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLOLSFGLTLMQII
                                                                                                                                                                                                                                           STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                 70;
                                502;
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                                                                 Indels
                                  Length
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                             ; Score 1246; DB 7;
; Pred. No. 3.1e-115;
86; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Protein NP_000737, SEQ ID NO 12739.
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                                46.8%;
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                   Conservative
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                                                Similarity
Sequence 502 AA;
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                                                                   Matches 240;
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                                  Query Match
                                                    Local
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ADD47051
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Costigan M; Befort K, D'urso D, WPI; 2003-268312/26 GENBANK; NP 000737 Woolf C,

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector, a method for identifying a mucleotide, a host cell comprising the vector, a method for identifying a mucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that invention discloses a composition comprising two or more isolated rat modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published pct sequences.

Sequence 502 AA;

241 CVLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300 DVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131 VPPPPDLELRERSSKSLLANVLD 392 STYPINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191 192 DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP 251 CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311 393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE 452 12 APAGLLILLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQII 71 4 SPGGVWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIM 63 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH---Gaps 312 MFMVASSVVSTILIINYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG------10; Length 502; 46.8%; Score 1246; DB 7; Length 5(46.0%; Pred. No. 3.1e-115; live 86; Mismatches 126; Indels Query Match Best Local Similarity 46.09 Matches 240; Conservative 252 72 64 132 184 361 qq g Dp qq ΩP δ qq ò à ò a ò δ

-DPDLAKILEEVRYIANRFRCQDE 452	494	494
417 -DEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDE 452	453 DADISRDWKFAAMVVDRLCLIFFTLFTIATLAVLLSAPHIM 494	453 SEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
- -DEHLLH	DADISRDWI	SEAVCSEW
417	453	453
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7, 2004, 11:35:48 Search completed: May 'Job time: 44.6667 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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No.
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-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Gen2_1/USFTO_spool/US09303232/runat_07052004_101110_23883/app_query.fasta_1.2261_0=(-Gen2_1/USFTO_spool/US09303232/runat_07052004_101110_23883/app_query.fasta_1.2261_0=(-Gen2_1/USFTO_spool/USFSTapp_-SUPFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-DOCALIGG=20.0 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGH=15 -MODE=LOCAL
-OURTEMT=pct -NORM=ext -HEAFSIZE=500 -MINIEN=0 -MAXLEN=2000000000
-USER=US09303232_@CGN 1 1_8225_@runat_07052004_101110_23883 -NCFU=6 -ICFU=3
-NO MMAP -LARREQUERY -NEG SCORES=0 -WAIT -DSPRICK=100 -LONGLOG
-DSW_TIMEOUT=120 -WARN -NIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPDFXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -FGAPOP=6
                                                                                                                8, 2004, 06:45:49 ; Search time 5459.09 Seconds (without alignments) 3938.047 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                    nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Perfect :
                                                                                                                     Run on:
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AY247962 Danio rer X52235 Chicken alp AY29875 Takifugu L37663 Mus musculu AR25596 Mus muscu AR05525 Sequence AR071403 Sequence

AF225980 AR055255 AR071403

AY298752 MUSNARS

AR173187 AR224030

AR282833

U40583 Human alpha L31619 Rattus ratt L25827 Human a7 ni

X70297 H. sapiens m

HUMA7NAR AX054575 AY299465

HSARA7A

HSU40583

Sequence Takifugu

AX054575 AY299465

AF486623 Macaca mu S53987 nicotinic

ALIGNMENTS

H.sapiens m

HSNACHRA7

AX054567

AR261850 AF385585

AX054567 Sequence Y08420 H.sapiens

Sequence Variant h

AR261850 : BD023656 T

AF385585 Homo sap:

AX719088 Sequence U62436 Human nicot

AR173187 Sequence AR224030 Sequence AR282833 Sequence

AF321446 Drosophil AF321447 Drosophil AJ524209 Drosophil BT011147 Drosophil AF321445 Drosophil AF321449 Drosophil AF321449 Drosophil AF33664 Drosophil AF36866 G.gallus mR

AF321447 DME554209

AF321446

AY036614 GGNNARA7A AY247962 GGA7NAREC

AF321448 AF321449

AF321445

BT011147

AX009610 Sequence AF143847 Heliothis

E58347 Nucleic ac AF272778 Drosophi AJ554210 Drosophi AY036613 Drosophi E58346 Nucleic ac:

DME554210

AX009610

AF143847

SUMMARIES

E58348 Nucleic aci AX009614 Sequence

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120

694 140 754 160 814 180 874 200 934 220 994 240

100 634

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ArgVallleThrAspGlnMetArgLysAspAspGluAspAlaAspIleSerArgAspTrp 460
     IleThrAsnIleTrpLeuLysLeuGluTrpAsnAspMetAsnLeuArgTrpAsnThrSer
                                                                                                            AspPheGlyGlyValLysAspLeuArgValProProHisArgLeuTrpLysProAspVal
                                                                                                                                                                                                                                                            CGGAACAACGCTCGTGTCTGTACGTGCCGCCCGGCATCTTCAAGAGCACCTGCAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                  AsplleThrTrpPheProPheAspAspGlnArgCysGluMetLysPheGlySerTrpThr
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                                                                                                                                                                GATTTCGGCCGGGTCAAAGATTTAAGAGTGCCACCCCACAGACTATGGAAACCAGACGTC
                                                                                                                                                                                                               LeuMetTyrAsnSerAlaAspGluGlyPheAspSerThrTyrProThrAsnValValVal
                                                                                                                                                                                                                                                                                                                            ArgAsnAsnGlySerCysLeuTyrValProProGlyIlePheLysSerThrCysLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACATCACCTGGTTCCCCTTCGACGACGATGCGAGGATGAAGTTTGGCAGCTGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1055 ACGCTCTACTACTTCTTCAATCTGATCGTGCCCTGCGTGCTCATCGCCTCCATGGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 LeuGlyPheThrLeuProProAspSerGlyGluLysLeuSerLeuGlyValThrIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuSerLeuThrValPheLeuAsnMetValAlaGluThrMetProAlaThrSerAspAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValProLeuLeuGlyThrTyrPheAsnCysIleMetPheMetValAlaSerSerValVal
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DDDFRHPQAQQPQCCXYYRGGEBNGAGLAARSCFGVDYELSLILKSRSYSTLINDWRKD
DEDADISRDWKFAAMVVDRLCLIFTLFTITATLAVLLSAPHINVS"
                        AF143846 3629 bp mRNA linear INV 27-MAY-1999 Heliothis virescens putative nicotinic acetylcholine receptor alpha 7-1 subunit mRNA, complete cds.
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/product="putative nicotinic acetylcholine receptor alpha
7-1 subunit"
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                                                                                                                                                                           Heliothis virescens (tobacco budworm)
Heliothis virescens
Heliothis virescens
Bukaryota, Metazaa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera; Glossata, Dirrysia,
Noctuoidea, Noctuidae, Heliothinae, Heliothis.

1 (bases 1 to 3629)
Schulte,T., Oellers,N. and Adamczewski,M.
Putative alpha subunits of insect nicotinic acetylcholine recept
more similar to vertebrate alpha 7 subunits and C. elegans Ce21
than to other insect nicotinic acetylcholine recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTCCTTCGGCCTCACGCTCATGCACATCATCGACGTGGACGAGGAGGAGGAGCAGCTTTTA
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Matches:
Conservative:
Mismatches:
Indels:
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/organia="Heliothis virescens"
/mol_type="mRNA"
/db_xref="taxon:7102"
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/note="hvnachra7-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
2 (bases 1 to 3629)
Schulte,T., Oellers,N. and
Direct Submission
Submitted (19-APR-1999) Zl
51368, Germany
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		181 TyraspGlyTyrGlnLeukspLeuGlnLeuGlnAspGluGlyGlyGlyGlyBsplleSerSer 200 875 TalGarGGTTATCAGTTGGATCTACAGTACAGGATGAAGGGGGGGG	41 ThrLeutyrTyrPhePheAsnieulleValProCysValLeulleAlaSerMetAlaLeu 55 AGGTCTACTACTTCTTCAATCTGATCGTGCCCTGCGTGCTCATCGCCTCCATGGCTCTTA 61 LeuGlyPheThrLeuProProAspSerGlyGluLysLeuSerLeuGlyValThrIleLeu 62 LeuGlyPheThrLeuProAspSerGlyGluLysLeuSerLeuGlyValThrIleLeu 63 LeuSerLeuThrValPheLeuAsnMetValAlaGluThrMetProAlaThrSerAspAla 64 LeuSerLeuThrValPheLeuAsnMetValAlaGluThrMetProAlaThrSerAspAla 65 CTGTCGTTGACGTGTTCCTCAACATGGTGGGGGAGGCGAGGGGGGCGCCGCCGCCCCCCCC	GIGCCCTIGCTCGGCACCTACTICAACTGCATCATGTTCATGGTGGCTTCCTCCGTCGTC 12 SerThrIleLeulleLeuasnTyrHisHisArgHisAlaAspThrHisGluMetSerAsp 34 ICCACCATACTGATCCTCAACTACCACCGGCACACGCAGACACTCACGAAATGAGTGGT 13 TrpIleArgCysValPheLeuTyrTrpLeuProTrpValLeuArgMetSerArgProGly 36 TGGATTGGTGGCGTGTTCCTTTATTGGCTGCCGTGGGTGCTGCGCATGTCACGGCCCGGC 14	361 SerAlaThrThrProProProAlaArgValProProArspLeuGluLeuhrgGlu 380 1415 TCGGCGACGCCGCCGCGCGCGCGCGCCGCCGCCGCACCTGGACTGCGCGAG 381 ArgSerSerLysSerLeuLeuAlaAsnValLeuAspIleAspAspAspPheArgHisPro 400 1475 CGCTCCTCCAAGTCGCTCTGAGCGACGTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
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	RESULT 2 AX009612 LOCUS AX009612 LOCUS AX009612 AX009612 AX009612 ACCESSION AX009612 VERSION AX009612. GI:9996844 KEYNORDS KEYNORDS REJIOTHIS virescens (tobacco budworm) ORGANISM Heliothis virescens Eukaryota; Matazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopteraryota; Arthropoda; Hespidoptera; Olossata; Ditrysia;	REFERENCE 1 ACTUOIDES, Moctunidae; Heliothinae; Heliothis. AUTHORS Adamczewski, M.D., Schulte, T.D. and Oellers, N.D. TITLE Nucleic acids encoding acetylcholin-receptor subunits from insects JOURNAL Patent: EP 0862528-A 3 08-DEC-1999; FRATURES Location/Qualifiers Source /organism="Heliothis virescens" Mol type="unassigned DNA" Ab xref="taxon:7102"	/ note / codo / codo / db_x / db_x / tran /	Ment Scores: No.: nt Similarity: Local Similarity Match:	US-09-303-232-4 (1-496) x AX009612 (1-3700) Oy

515 CTCTCCTTCGGCCTCATGCAGATCATCGACGTGGACGAGAACCAGCTTTTA 574 81 IleThrAsnIleTrpLeuLysLeuGluTrpAsnAspMetAsnLeuArgTrpAsnThrSer 100		875 TATGATGGTTATCAGTTGGATCTACAGGATGAAGGGGGGGG		1235 GIGCCCTIGCTCGGCACCTACTTCAACTGCATCATGGTGGTGGCGTCCTCCGTCGTC 1294	SerAlaThrThrProProProAlaArgValProProProAspLeuGluLeuArgGlu TCGGCGACGACGCCGCCGCCGCCGCCGCGGACCTGGAGCTGCGCGGAG ArgSerSerLysSerleuLeuAlaAsnValLeuAspIleAspAspAspAspPheArgHisPro GCTCCTCCAAGTCGCTCCAGCGACGTGCTCGACCTCGAGCTCCGCGAG GIDALAGINGINProGInCysCysArgTyrTyrArgGlyGluGluAsnGlyAlaGly CAAGCCCAGCTCCTCCAAGTCGTCCCTGCGCAGCGCGCGC
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	8 8 8 8 8	8 6 8 6 8 6 8	7 8 8 8 7	4 6 6 6	888888
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LSAPHIIVS"
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                                                                                                                                                                                                                                                                                                              'note="results in threonine to isoleucine substitution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuLeuLeuLeuCysLeuLeuTrpProArgGlyAlaArgCysGlyTyrHisGluLysArg
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/note="results in asparagine to serine substitution;
compared to B allele"
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                                                                                                                                                                                                        isoleucine
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| Gene="mbooksalpha-34E"
|note="results in deletion of asparagine
compared to B allele"
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396
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/note="results in phenylalanine to
substitution; compared to B allele"
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Matches:
Conservative:
Mismatches:
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                                                                                          /gene="nAcRalpha-34E"
/note="compared to B allele"
/replace="a"
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/gene="nAcRalpha-34E"
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NMLSPKTAAAATAAGDEATTQOPTNIRLCARKRQRLRRRRKRKPATPNETDIKKQQQL
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IWKPDVLMYNSADEGFDGTYQTNVVVNNNGSCLYVPPGIFKSTCKIDITWFPFDDQRC
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LCWLPWILRNGRPGFRELILEFPTTPCSGTSSRRKHQILSDVELKERSSKSLLANVLDI
                                                                                                                                                                                                                                                                                                                                       AF272778 2907 bp mRNA linear INV 29-APR-2002
Drosophila melanogaster nicotinic acetylcholine receptor Dalpha5
subunit (nAcRalpha-34E) mRNA, nAcRalpha-34E-A allele, complete cds.
AF272778
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      1595 TTGGCGGCGCACAGTTGCTTCGGTGTCGACTACGAGCTCTCCCTCATTCTGAAGGAGATT 1654
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                     461 LysPheAlaAlaMetValValAspArgLeuCysLeuIleIlePheThrLeuPheThrIle
                                               ArgValIleThrAspGlnMetArgLysAspAspGluAspAlaAspIleSerArgAspTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FGU, University of Oxford, South Park Road, Oxford OX1 3QX, UK Location/Qualifiers
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/note="ion channel; neurotransmitter transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2907)
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/db_xref="taxon:7227"
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1. .2907
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Grauso, M. and Sattelle, D.B.
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UDRLCIIFTLFTIIATLAVLFSAPPHFIVSGVRG"
 INV 01-APR-2003
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                                                                                                                                      DMES54210 1683 bp mRNA linear INV 01-APR-200 Drosophila melanogaster mRNA for nicotinic acetylcholine receptor subunit Dalpha7 (nAcRalpha-18C gene).
                                                                                                                                                                                                                                                                                                                                                          .S., Department of Pharmacology, Street, London, WCIE 6BT, UNITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GlyGlyArgAlaArgArgSerHisLeuAlaAlaProAlaGlyLeuLeuLeuLeuCys
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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nAcRalpha-18C gene; nicotinic acetylcholine receptor subunit
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Dalpha7"
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                                                                                                                     GlySerTrpThrTyrAspGlyTyrGlnLeuAspLeuGlnLeuGlnAspGluGlyGlyGly
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AY036613 2834 bp mRNA linear INV 30-APR-2002 Drosophila melanogaster nicotinic acetylcholine receptor Dalpha5 subunit (nAcRalpha34E) mRNA, nAcRalpha34E-B allele, complete cds,
                                                                                                                                                                                                                                      TCCGGCGAGAAGAAGCAACAGATCCAAAAGGTTGAGCTCAAGGAGAGGGTCCTCCAAGTCT 1231
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                                                             CTGCTGGCCAATGTGCTCGATATAGACGATGATTTCCGATGCAATCATCGATGTGCCAGC
                                                                                                                                                                                                                                                                                               AlaHisSerCysPhe-----GlyValAspTyrGluLeuSerLeuIleLeuLysGluIle
                                            LeuLeuAlaAsnValLeuAspIleAspAspAspPheArg-----HisProGlnAla---
                                                                                                    ------GlnglnProGlnCysCysArg---TyrTyrArgGlyGlyGluGluAsn
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Grauso, M. and Sattelle, D.B.
Grauso, M. and Sattelle, D.B.
Submitted Submission
University of Oxford, South Parks Road, Oxford OX1 3QX, UK
Location/Qualifiers
I. 2844
/ organism="Drosophila melanogaster"
/ Mol Lype="mRNA"
/ db xref="taxon:7227"
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/note="ion channel; neurotransmitter transmembrane
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygot
Bobptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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receptor; exon 5 is excluded due to exon skipping, generates a loss of reading frame and a truncated polypeptide, alternatively spliced" /codon start=1 /product="nicotinic acetylcholine receptor Dalpha5
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     AsnGlulleTyrTyrAsnCysCysProGluProTyrIleAspIleThrPheAlaValVal
                                                   237 IleArgArgLysThrLeuTyrTyrPhePheAsnLeuIleValProCysValLeuIleAla
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                                               Drosophila melanogaster
JP 2000023680-A/1
25-JAN-2000
26-APR-1999 JP 1999118159
04-MAY-1998 DE 19819829.9
MARTIN ADAMUTSUEUSUKI,NADJA ERASU,THOMAS SCHULTE PC
 Martin, A., Nadja, E. and Thomas, S.
Nucleic acid encoding insect actyl choline receptor subunit
Patent: JP 2000023680-A 1 25-JAN-2000;
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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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Neoptera; Endopterygota; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                           Auchiczewski,M.D., Schulte,T.D. and Oellers,N.D. Nucleic acids encoding acetylcholin-receptor subunits Patent: BP 0962528-A 1 08-DEC-1999; BAYER AG (DE)
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361
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/organism="Drosophila melanogaster"
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/db_xref="taxon:7227"
372. .2684
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Matches:
Conservative:
Mismatches:
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/note="unnamed protein product"
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db xref="G1:9996843"

db_xref="REMTREMBL:CAC07499"
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TGGATACTGCGAATGTCGAGGCCAGGGAAGAAGATCACCAGGAAGACTATAATGATGAAC
                                                                                                                                              AspMetAsnLeuArgTrpAsnThrSerAspPheGlyGlyValLysAspLeuArgValPro 111
                                                                                                                                                                                                                                                                                                                GGGACCTACCAGACCAACGTGGTCAGAAGCGGCGCGCAGTTGCCTGTACGTGCCACCT 514
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                                                                                                                                                                                                                                                                                                                                                              GlyllePheLysSerThrCysLysIleAspIleThrTrpPheProPheAspAspGlnArg 171
                                                                                                                                                                                                                                                                                                                                                                               CysGluMetLysPheGlySerTrpThrTyrAspGlyTyrGlnLeuAspLeuGlnLeuGln 191
                                                                                                                                                                                                                                                                                        SerThrTyrProThrAshValValValArgAsnAshGlySerCysLeuTyrValProPro 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspValAspGluLysAsnGlnLeuLeuIleThrAsnIleTrpLeuLysLeuGluTrpAsn
                                                                                                                                                                                                                    ProHisArgleuTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValProglyLysArgAsnGlulleTyrTyrAsnCysCysProgluProTyrIleAspIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAACTCACACTTGGAGTCACTATTCTTCTTTCGCTGACGGTGTTCCTCAAACCTGGTAGCC
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                                                                                                           GACGEGGACGAGAATCAACTACTTATAACCAATATATGGCTGTCGTTGGAGTGGAAT
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NLVAETLEQVSDAIPLLGYFFNLIVENNASSVVLTVVVLNYHHRTADIHEMPQMIKSV
FLQMLPWILLSMRSPGKKITRKTIMMYTRABLELEKRRSSKSLADNULDIDDFRHGGP
PPNSTASTGNLGPGCSIFRTDFRRSFVRESTWEBVGGGGLGSHHRELHILLRELGFITA
RMKKADEEABLISDWKFAAMVUDRFCLFVFTLFTILTATVAVLLSAPHIIVQ"
                                                                                                                                                                                                                                                                                                   Schulte, T., Oellers, N. and Adamczewski, M.
Putative alpha subunits of insect nicotinic acetylcholine receptors
more similar to vertebrate alpha 7 subunits and C. elegans Ce21
than to other insect nicotinic acetylcholine receptor alpha
                                                                                 AF143847

3029 bp mRNA linear INV 27-MAY-1999
Heliothis virescens putative nicotinic acetylcholine receptor alpha
7-2 subunit mRNA, complete cds.
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/product="putative nicotinic acetylcholine receptor alpha
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                                                                                                                                                                                   Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.

I (bases I to 3029)
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Schulte,T., Oellers,N. and Adamczewski,M.
Direct Submission
Submitted (19-APR-1999) ZF-BTB, Bayer AG,
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/db_xref="taxon:7102"
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TITLE
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JOURNAL
                                                                                                                                          ACCESSION
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Qy 18	Db 275 GACGTGGACGAGAATCAACTACTATAACCAATAATGCTGCTGCGAGTGGAAT 334 Qy 92 AspWetAsnleuArgTrpAsnThrSerAspPheGlyGlyValLysAspLeuArgValPro 111 Db 335 GACTACAACTGAGGTGGAACGACTATGGCGGGTCAAGGACCTCAGGATCACG 394 Qy 112 ProHisArgLeuTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAsp 131 Db 395 CCCAACAAGTTGGGAAGCCGGACTATGTATGATGATGAGGAGGTTTTGAC 454 Oy 132 SerThrTyrProThrAsnJaValValArgAshAsnGAJYSerCysLeuTyrValProPro 151	455 GGGACCTACCAGACCAGAGGGGGGGGGGGGGCGGCGGCGGCGCCGCC	Cy Aspoint-Motyvap in the server in the short in the shor	Db 815 IGCGTGGTGTTCTCATCGATGGCATCCTCGCGTCACCACCGACACACGAGAGA 874 Qy 272 LysLeuSerLeuGlyvalThrileLeuLeuSerLeuThrValPheLeuAsnMetValAla 291 Db 875 AAACTCACACTTGGAGTCATATCTTCTATCGCTGACGATCCTAACTTGTAGCC 934 Qy 292 GluThrMetProAlaThrSerAspAlaValProLeuLeuGlyThrTyrPheAsnCygla 311 Db 935 GAGACCTGCCACAGGTCTCCGGGCTTACCTCAACTTCAATGCATC 994	312 MetPheMetValAlaSerSerValValSerThrIleLeuIleLeuAsnTyrHisHisArg
	471 CysleulleilePheThrLeuPheThrIeileAlaThrLeuAlaValLeuLeuS	ITION SION ON RDS E ANISM ENCE	ACHORN MICHEL ACTIONS TO TITLE NUCLEIC acid encoding insect actyl choline receptor subunit Patent: JP 2000023680-A 3 25-JAN-2000; BAYER AG COMMENT DA 2000023680-A 3 25-JAN-2000; COMMENT DA 1000023680-A/3 PD 25-JAN-2000 PD 25-JAN-2000 PP 26-JAN-2000 PP 26-JAN-2000 PR 04-MAY-1998 DE 19819829.9 PR 04-MAY-1998 DE 19819829.9 PR MARTIN ADAMUTSUBGSUK, NADJA ERASU, THOMAS SCHULTE PC CL2NIS/09, A01K67/033, CO7K14/705, CO7K16/28, CL2NI/21, CL2NS/10, PC CL2NI/68, PC G01N33/15, G01N33/50// (C12NI/21, C12R1:19), CL2NIS/00, CL2NIS/00 CC	FH Key Location/Qualifiers FEATURES (95)(1597). source 13109 /organism="Heliothis virescens" /mol_type="genomic DNA" /db_xref="taxon:7102"	Alignment Scores:

Percent Similarity: 77.52* Conservative: 55 Best Local Similarity: 67.05* Mismatches: 78 Query Match: 67.88* Indels: 40 Bs: 6 Gaps: 8 US-09-303-232-4 (1-496) x AX009614 (1-3109) Qy 5 AlaArgArgSerHisLeuAlaAlaProAlaGlyLeuLeu	Db 38 GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	Oy 32 TyrHisGluLysArgLeuLeuHisHisLeuLeuAspHisTyrAsnValLeuGluArgPro 51 Db 155 CCTCACGAGAAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACGC 214	Qy 52 ValValAsnGluSerAspProLeuGlnLeuSerPheGlyLeuThrLeuMetGlnIleIle 71 Db 215 GTGGCCAACGAGGGACGCTAGAGGTTCGGCTTGACCTTGCAGCAACCATA 274	Qy 72 AspValAspGluLysAsnGlnLeuLeuLlethrAsnIleTrpLeuLysLeuGluTrpAsn 91 Db 275 GACGTGGACGAGAAGAATCAACTACTATAAACCAATATATGGCTGTCGTTGGAGTGGAAT 334	QY 92 AspMetAsnLeuArgTrpAsnThrSerAspPheGlyGlyValLysAspLeuArgValPro 111 Db 335 GACTACAACCTGAGGACACAGCGAGTATGGCGGGGTCAAGGACCTCAGGATCACG 394	112 ProHisArgLeuTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAsp ::::::	Qy 132 SerThrTyrProThrAsnValValValvalArgAsnAsnGlySerCysLeuTyrValProPro 151 Db 455 GGGACCTACCAGACCAACGTGGTGCTCAGAAGCGGCGGCGGCAGTTGCCTGTACGTGCCACT 514	Qy 152 GlyllePheLysSerThrCysLysIleAsplleThrTrpPheProPheAspAspGlnArg 171	Oy 172 CysGluMetLysPheGlySerTrpThrTyrAspGlyTyrGlnLeuAspLeuGlnLeuGln 191 [:::	Oy 192 AspGluGlyGlyGlyAspIleSerSerPheValThrAsnGlyGluTrpGluLeuIleGly 211	Qy 212 ValProGlyLysArgAsnGluIleTyrTyrAsnCysCysProGluProTyrIleAspIle 231 :::	Qy 232 ThrPheAlaValValIleArgArgLysThrLeuTyrTyrPhePheAsnLeuIleValPro 251	Qy 252 CysValLeullealaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGlu 271	Qy 272 lysLeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAla 291 Db 875 AAACTCACACTIGGAGTCACTATCTTCTATCGCTGACGGTGTTCCTCAACCTGGTAGCC 934	Qy 292 GlufhrMetProAlaThrSerAspAlaValProLeuLeuGlyThrTyrPheAsnCysIle 311 Db 935 GAGACCCTACAGGTCACCAGCTAACCCCTATCAGGCGAACCTAACCAGC	312 MetPheMetValAlaSerSerValValSerThr11eLeu11eLeuAsnTyrHisHisArg 33
1175 ACGAGGATGAGGAGCTGAACTGAAGGACGACCTTGCTTGC	Db 1295 GGGAAITIGGGA[Qy 431 TyrGluLeuSerLeuIleLeuLysGluIleArgValIleThrAspGlnMetArgLysAsp 450	Oy 451 AspGluAspAlaAspIleSerArgAspTrpLysPheAlaAlaMetValValAspArgLeu 470	Oy 471 CysleullellePheThrLeuPheThrIlelleAlaThrLeuAlaValLeuLeuSerAla 490	Oy 491 ProHisIleMetVal 495 	AX009614 LOCUS AX009614 3109 bp DNA linear PAT 06-SEP-2000 DEFINITION Sequence 5 from Patent EP0962528.	ACCESSION AXUU9614 VERSION AXU09614.1 GI:9996846 KEYWORDS Haliothic wirecomm (tobacce)	Heliothis virescens Eukaryota; Metazoa; Neoptera; Endopteryg	REFERENCE 1 AUTHORS Adamczewski, M.D., Schulte, T.D. and Oellers, N.D. TITLE Nucleic acids encoding acetylcholin-receptor subunits from insects JOURNAL Patent: EP 0962528-A 5 08-DEC-1999,	BAYER AG (DE) FEATURES Location/Qualifiers Source 13109		/note intimated protein product / codon start=1 / protein_id="CAC07501.1" / db xref="dT:9956847" / db xref="nT:9956847" / db xref="nT:995	AT THE WASHINGTON OF SOME AND	DVTFTIMIRRATIVYEENLIVPEVALISASALASTATANGATILATITAVEEPIV DVTFTIMIRRATIVYEENLIVPEVALISASALASTATAVATHIRTADIHEMPQMIKSV FLQMLDWIILBARSPEKKITRKIILMMYRRARELEIKERSSSSLLANVIDIDDDPRHGGP PDNRTRASTGANIGAGS IRPUIDEDE SVIDE SCHARANIVAGATIGATILATADIHEMPGPP		Alignment Scores: 2.4e-164 Length: 3109 Pred. No.: 2.4e-164 Matches: 352

us-09-303-232-4.rge

and 8a"

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variant type II"

'protein id="AAM13393.1"

/db xref=""G1:20152847"

/translation="MDSPLPASLSIFVLLIFLAIIKESCQGPHEKRLLNHLLSTYNTL

FRYANDESPEDFWKFGLTTQQIIDVDVENQLLIFTNIMJLSENADDYNLANDESFGGWK

DLRITPNKLWKFDVLAWTNSADEGFDGTYHTNIVVKHGGSCLIVVPPGTFKSTCKGDITW

FPFDDQHCEMKFGSWTYDGNQLDLVLNSEDGGDLSDFITNGEWYLLAMPGKKNTIVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSLTVFLNLVAESMPTTSDAVPLIGTYFNCIMFMVASSVVLTVVVLNYHRTAIHEM
PPWIKSVFLQWLPWILRMGRPGRKITRKTILLSNRMKELELKERSSKSLLANVLDIDD
DFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELQFITARMRKADD
BAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ"
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/note="results in glycine to serine substitution; compared
to variant clone"
                                                                                                                                                                                                                                                        /codon_start=1
/product="nicotinic acetylcholine receptor Dalpha6 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                           CCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
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//gene="nAcRalpha-30D"
/note="results in glycine to asparagine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="results in asparagine to serine substitution; compared to the sequence deposited in GenBank Accession Number AE003626 and in variant clone"
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                                                                                                                                                                                                            /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3b
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organism="Drosophila melanogaster"
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'replace="t"
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/replace="t"
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/note="compared to variant clone"
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                     /mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                      dev stage="embryo" . .2023
                                         db_xref="taxon/chromosome="2"
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1460 GATGAGGAAGCCGAGCTGATCAGCGACTTGCTGCGATGGTTGTTGATAGTTT 1519
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalphar, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
3QX, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 TyrGluLeuSerLeuIleLeuLysGluIleArgValIleThrAspGlnMetArgLysAsp
                                                                                  1055 ACAGCTGATATACATGAAATGCCACAGTGGATAAAATCAGTATTCCTACAATGGTTGCCA
                                                                                                                            TrpValLeuArgMetSerArgProGlySerAlaThrThrProProAlaArgVal---
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                                             HisAlaAspThrHisGluMetSerAspTrpIleArgCysValPheLeuTyrTrpLeuPro
                                                                                                                                                                                                                                                                                               Leuaspileaspasspanghis-----proglnalagingin----
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                ----ProGlnCysCysArgTyr-----TyrArgGlyGly---
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1. .2023
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subunit variant type II
alternatively spliced.
AF321446
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphae and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-1 Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                        SerLeulleLeulysGlulleArgValIleThrAspGlnMetArgLysAspAspGluAsp
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|GGGAATTGATCGGCGATTGGAAGTTCGCGGCAATGGTTGTGGTTGTTTTGTTTAATT
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopteray; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford (
30X, UK
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/note="ion channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3b
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/protein_id="AAM13394.1"
/db xref="GI:20152849"
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/organism="Drosophila
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BRPVANESBPLEVKFGLTLQQIIDVDEKNQLLITNLMLSLEMNDYNLKWNETEYGGVK
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CCPEPYVDITFIIQIRRRILYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
                                                                         LSLTVPLALVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVVLINYHHRTADIHEM PPWIKSVFJCAMLPWILEMRERSKSLLANVLDIDD PPWIKSVFJCARRESSKSELANVLDIDD DFRHTI SGSQTAIBSSASFGRPTTVEEHHTALGCNHKDLHLILKELQFITARMRKADD EAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ**
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compared to the sequence deposited in GenBank Accession
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                              GATCTACGAATCACGCCCAACAAGCTCTGGAAGCCCGACGTGCTCATGTACAACAGCGCG
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EABLIGDWIKFAAMVUDRFCLIVFTLETIIATVTVLLISAPHIIUU"
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                                                                                                                                                                                      .S., Department of Pharmacology,
Street, London, WCIE 6BT, UNITED
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Weoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/product="nicotinic acetylcholine receptor subunit
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/product="nicotinic acetylcholine receptor subunit
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Matches:
Conservative:
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Direct Submission
Submitted (31-MAR-2003) Millar N.
University College London, Gower
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PGIFKSTCKMDITWFPFDDQHCEMKFGSWTYDGNQLDLVLSSEDGGDLSDFITNGEWY
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Stableton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Stableton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
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1397 GCGGAATTGATCGGCGATTGGAAGTTCGCGGCAATGGTTGTGGATAGATTTTGTTTAATT 1456
                                                                       474 IlePheThrLeuPheThrIleIleAlaThrLeuAlaValLeuLeuSerAlaProHisIle
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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full insert cDNA.
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/mol_type="mRNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
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Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
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Drosophila melanogaster (fruit fly)
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/db_xref="GI:40216008"
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/codon_start=2
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PDSGEKLTLGYTILLSLTVFINLVAESMPTTSDAVPLIGTYFNCIMFMVASSVVITTVV
VLNYHRTADIHEMPPWIKSVFLQWLPWILRMGRPGRKITRKTILLSNRMKELELKER
SSKSLLANVLDIDDDFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILK
BLQFITARMRKADDEAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ
LLAMPGKKNTIVYACCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTLP
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AsnLeulleValProCysValLeulleAlaSerMetAlaLeuLeuGlyPheThrLeuPro

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ProAspSerGlyGluLysLeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPhe

CCGGATTCGGGCGAGAAACTGACGTGGCGTAACTATACTATCATTAACAGTATTT

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TyrPheAsnCysIleMetPheMetValAlaSerSerValValSerThrIleLeuIleLeu 326
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                                                                                                                       347 LeuTyrTrpLeuProTrpValLeuArgMetSerArgProGlySerAlaThrThrProPro 366
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Chimeric Modified

Human pol Drosophil

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Abl10279
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Abs5487
Abd2062
Ada10856
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Abbs73243
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Ada10854
Abbs73247

Neuronal

Prostate
Human neu
Human 205
Human 205
Modified
Modified
Human CHR
Drosophil

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AAT48236
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AAV12199
AAQ90387
ABS54870
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ADA10854
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    Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/CGR21 / USG930323/Trunat 07052004 101109 23873/app query.fasta_1.2261
-Q=/CGR21 / USGPFO spool/30323/Trunat 07052004 101109 23873/app query.fasta_1.2261
-DB=N Geneseq 29Jan04 - OFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITX=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-UST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-UST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_PAPEIZE=S00 -MINLENG -MAXLEN=2000000000
-USER=US0930323 -GCR0 1 1.1200 @runat -07052004 101109 23873 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMBOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                          ; Search time 520.982 Seconds
  (without alignments)
  4044.486 Million cell updates/sec
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            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                  - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                             Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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1 MGGRARRSHLAAPAGLLLLL.
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1: geneseqn1980s:*
2: geneseqn1990s:*
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length: 2000000000
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                              Copyright
                                                                                                                            May
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Minimum DB seq Maximum DB seq

Searched:

Perfect score:

Sequence:

protein

Run on:

Scoring table:

Human neu Drosophil Neuronal

Human neu

Neuronal Human

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Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds.
                                                     H. virescens acetyl-choline receptor DNA from clone Hva7-1.
                                                                                                                                      /*tag= a
/product= "acetyl-choline receptor"
AAZ24476 standard; cDNA to mRNA; 3700 BP
                                                                                                                   Location/Qualifiers 335. .1825
                                                                                                                                                                                                    98DE-01019829
                                                                                                                                                                                                                      98DE-01019829
                                                                                                 Heliothis virescens.
                                                                                                                                                                DE19819829-A1
                                                                                                                                                                                                                      04-MAY-1998;
                                                                                                                                                                                                    04-MAY-1998;
                                                                                                                                                                                  11-NOV-1999
                  AAZ24476;
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Adamczewski M, Oellers N, Schulte T;

(FARB) BAYER AG

D. melano H. viresc Drosophil Drosophil Neuronal

Aaz24475 I Aaz24477 I Abl07231 I Abl13733 I Aat59196 I Aav12197 I Aat48239 I

ABL07231 ABL13733 AAT59196 AAV12197 AAT48239

3700 2886 3109 1540 936 2769 1876

2665 1850 1809 1623.5 1417.5 1267 1247

12645978

67.9 60.9 53.2 47.5 46.8

Aaz24476 H. vireso

AAZ24476 AAZ24475 AAZ24477

100.0

Query Match Length DB

Score

Result No.

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:*

Database

geneseqn2002s:*

geneseqn2003bs:* geneseqn2003cs:* geneseqn2003as:*

geneseqn2004s:*

Human neu Neuronal

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                                                                                                                                                                   This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere with neurotransmission. (1) (also vectors containing it, its regulatory regions, and antibodies directed against (1)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline
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                                                           nucleic acid encoding a nicotinic acetylcholine receptor from sets, used to identify potential insecticides.
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                     2574 AAATTTGCAGCTATGGTCGTTGACAGACTGTGCCTTATCATATTCACAATGTTCGCAATA 2633
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                                                                            TTAGCCACAATAGCTGTACTACTATCGGCACCACATATTATTGTCTCG 2681
                                                            IleAlaThrLeuAlaValLeuLeuSerAlaProHisIleMetValSer 496
                                                                                                                                                                                                                          H. virescens acetyl-choline receptor DNA from clone Hva7-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
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ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                               SerHisLeuAlaAlaProAlaGlyLeuLeuLeuLeuCysLeuLeuTrpProArgGly
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                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidaring cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175 and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                          detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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                                                                                                                                               + Sequence Listing; English.
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P-PSDB; ABB69630.
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                               AsnCysCysProGluProTyrIleAspIleThrPheAlaValIleArgArgLysThr
                                                                LeuTyrTyrPhePheAsnLeuIleValProCysValLeuIleAlaSerMetAlaLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated neuronal alpha-bungaro-toxin-binding protein DNA - used screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                binding protein alpha 1; cholinergic;
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2 cDNA clones (AAT59196 and AAT59197) respectively code for the alphal subunit (AAW12368) of chick neuronal alphabungarotoxin binding protein (ABBP). They were isolated from an 18-day embryo chick brain cDNA library using a probe (see also AAT59198) based

English

Claim 1; Fig 2A-B; 18pp;

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on the N-terminal amino acid sequence of chicken brain ABBP. The probe isolated partial clone pGDE29-1, which encoded the N-terminal portion of alphal. A subclone, pGD29-3 (ATCC 40641), was used to rescreen the library, yielding clone pGD3-1 (ATCC 40640), which encoded the enrire alpha2 sequence. A probe based on the C-terminal region of pGD3-1 was used obtain clone pCD3-1 (ATCC 40639), encoding the C-terminal portion of alpha1. The cDNA clones can be used as probes to identify further ABBP subunits, and in the recombinant prodn. of ABBP
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Matches:
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64.84%
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Best Local Similarity:
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receptor (NAChR) subunit. The cells expressing the alpha and/or beta NAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells that express a variety of subtypes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human neuronal nicotinic acetylcholine receptor subunits and DNA - also transformed cells useful for screening cpds. which modulate activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 ProArgGlyAlaArgCysGlyTyrHisGluLysArgLeuLeuHisHisLeuLeuAspHis
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TGGACAAGAGTCATCCTTCTGAATTGGTGTGCTTGGTTTCTGAGGATGAAGAGACCAGGG
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/product= "neuronal nicotinic acetylcholine receptor
alpha-7 subunit"
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                      SerAlaAspGluGlyPheAspSerThrTyrProThrAsnValValValArgAsnAsnGly
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GlnMetArgLysAspAspGluAspAlaAspIleSerArgAspTrpLysPheAlaAlaMet
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ligand-gated receptor; ds.
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P-PSDB; AAW09025.
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P-PSDB; ABG70492

Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to Identifying

57-60; 56pp; English Claim 101; Col

The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (NAVChNS), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents cDNA encoding the alpha 7 subunit of the human nNAChR polypeptide

T; 0 U; 1 Other; G; 423 530 ΰ 369 A; 553 Sequence 1876 BP;

1876 247 85 129 88 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: (1-1876)US-09-303-232-4 (1-496) x ABS54875 4.91e-115 1247.00 60.47% 44.99% 46.79% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell comprising nucleic acids encoding human alpha and beta subunits of neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans.
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'note= "neuronal nicotinic acetylcholine receptor"
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immunochemistry; NAChR alpha7 subunit; gene; ss.
                                                                                        neuronal NAChR alpha7 subunit encoding cDNA
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ProArgGlyAlaArgCysGlyTyrHisGluLysArgLeuLeuHisHisLeuLeuAsPHis
                                                                      CTGCACGTGTCCCTGCAAGGCGAGTTCCAGAGGAAGCTTTACAAGGAGCTGGTCAAGAAC
                                                                                                                                                TyrAsnValLeuGluArgProValValAsnGluSerAspProLeuGlnLeuSerPheGly
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                                                       LeuLeuAlaAsnValLeuAspIleAspAspAspPheArgHisProGlnAlaGlnGlnPro
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cgcttccgctgccagacgaagaagcggtctgcagcagcgagttcgccgcctgt
                                       ----ValProProProAspLeuGluLeuArgGluArgSerSerLysSer
                                                                                                                     406 GlnCysCysArgTyrTyrArgGlyGlyGluGluAsnGlyAlaGlyLeuAlaAlaHisSer
                                                                                                                                                             426 CysPheGlyValAspTyrGluLeuSerLeuIleLeuLysGluIleArgValIleThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                           ds; gene; alpha 7 subunit; human; neuronal nicotinic acetylcholine receptor; ligand-gated ion channel; synaptic transmission; gene therapy; transgenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding an alpha-6 or a beta-3 subunit of a human
                                                                                                                                                                                                                                                                                                                                                                                                             7 subunit
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ThrThrProProProAlaArg-
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P-PSDB; ADA10874.
                                                                                                                                                                                                                                                                                                                                               standard;
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nicotinic acetylcholine receptor (nAChR), useful for identifying
that modulate human neuronal nAChR activity.
                                                                  The invention relates to an isolated nucleic acid molecule comprising a neucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human neuronal nicotinic acetylcholine receptor naChR. nAChR's form ligandgated ion channels that mediate synaptic transmissions between nerve and muscle and between neurons upon interaction with the neurotransmitter compounds that modulate human neuronal naChR. The present sequence represents DNA encoding the human neuronal nicotinic acetylcholine receptor, nAChR, alpha 7 subunit. Note: the present sequence decodes to the protein shown in ADA10874 not the one described in the specification as being the nAChR alpha 7 subunit ADA10865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CTGCACGTGTCCCTGCAAGGGGAGTTCCAAGGATTACAAGGAGCTGGTCAAGAAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                            ---SerHisLeuAlaAla-
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                          67-72; 63pp; English
 acetylcholine
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neuronal
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1072 ATCCTTCTGAACTGGTGCGCGTGGTTCCTGCGAATGAAGGGCCCGGGGAGGACAAGGTG 1131
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                                                                                                                                                                                                                                                                                               --SerAla
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                                                                        PhePheAsnLeuIleValProCysValLeuIleAlaSerMetAlaLeuLeuGlyPheThr
                                                                                                                                                            772 GGCCTCAACCTGCTGATCCCCTGTGTGTGTTCTCCGCCCTCGCCCTGGCTGTTCCTG
                                                                                                             LeuProProAspSerGlyGluLysLeuSerLeuGlyValThrIleLeuLeuSerLeuThr
                                                                                                                      IleLeuAsnTyrHisHisArgHisAlaAspThrHisGluMetSerAspTrpIleArgCys
 GlyGluTrpGluLeuIleGlyValProGlyLysArgAsnGluIleTyrTyrAsnCysCys
                                     ProGluProTyrIleAspIleThrPheAlaValValIleArgArgLysThrLeuTyrTyr
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO355, PRO1025, PRO1030, PRO4019, PRO4019, PRO1025, PRO1030, PRO40197, PRO10197, PRO1197, PRO10197, PRO10184, PRO10187, PRO10184, PRO20184, PRO21987, PRO20198, PRO20198, PRO10184, PRO10184, PRO10184, PRO10187, PRO10184, PRO10184, PRO10187, and prevention of cancer. The antibodies and other anti-tumour compounds and prevention and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, conditions or disorders to be treated with such antibodies and other compounds, and various head and neck tumours), leukaemias and conformal and blastocoelic disorders, and inflammatory, angiogenic and etromal and blastocoelic disorders, and inflammatory, angiogenic and compounds inmunoledic disorders. AACS824C to AACS836 represent PRR primers and hybridisation probes used in the isolation of the human PRO sequences. Proceedant invention
                                                                                                                 Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glaal disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inmunologic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROY MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thirty PRO polymucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gurney AL,
                                                              PRO2145 nucleotide sequence SEQ ID NO:76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 50; Fig 57; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US012252.
99US-0141037P.
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99US-0145698P.
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Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
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(first
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Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-1999;
02-JUN-1999;
23-JUN-1999;
07-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JAN-2000;
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29-JAN-2001
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Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 U; 0 Other;

1509 240

Length: Matches:

4.5e-115 1246.00

Alignment Scores: Pred. No.: Score:

AAC58395 standard; cDNA; 1509

AAC58395;

Page 15

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cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
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Example 5; Page 60-61; 77pp; English.

The present sequence is the coding sequence for wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAG90382 and ABB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells

Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 U; 0 Other;

Aliqnment (Scores:			
. ಕ್ರಾಕ್ಟರ್ಗಳ	lar imi	4.5e-115 1246.00 62.45% 45.98% 46.75%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1509 240 86 1126 6
US-09-303-2	232-4 (1-496)	x AAC90380 (1-	-1509)	
ζ	laProAl	GlybeuLeuLeuLeu	leuCysleuleuTrp	aGlyLeuLeuLeuLeuLeuCysLeuLeuTrpProArgGlyAlaArgCysGly 31
qq	10 TCGCCGGGA	 GGCGTCTGGCTGGCC	 screececercerro	TCGCCGGGAGGCGTCTGGCTGGCGTGGCGGTCGCTCCTGCACGTGTCCCTGCAAGGC 69
δλ	32 TyrHisGlu	LysArgLeuLeuHis	SHisLeuLeuAspHis	TyrHisGluLysArgLeuLeuHisHisLeuLeuAspHisTyrAsnValLeuGluArgPro 51
Db	70 GAGITCCAG	GAGGAAGCTTTACAAC	SGAGCTGGTCAAGAAC	GAGTICCAGAGGAAGCITIACAAGGAGCIGGACAAAACTACAATACCTIGGAGAGGCCC 129
ζō	52 ValValAsn	GluSerAspProber	JGInLeuSerPheGly	alValAsnGluSerAspProLeuGlnLeuSerPheGlyLeuThrLeuMetGln11e11e 71
Dp	130 GTGGCCAAT	GACTCGCAACCACT	CACCGTCTACTTCTCC	GIGGCCAATGACTCGCAACCACCACCGTCTACTTCTCCCTGAGCCTCCTGCAGATCATG 189
λ̈́o	72 AspValAsp	GlubysAsnGluber	JeulleThrAsnile	AspValAspGluLysAsnGlnLeuLeulleThrAsnIleTrpLeuLysLeuGluTrpAsn 91
Db	190 GACGTGGAT	GAGAAGAACCAAGT	: TTAACCACCAACATT	GACGTGGATGAGAACCAAGTTTTAACCACCAACATTTGGCTGCAAATGTCTTGGACA 249
o. Võ	92 AspMetAsn	LeuargTrpasnTh	rSerAspPheGlyGly	AspMetAsnLeuArgTrpAsnThrSerAspPheGlyGlyValLysAspLeuArgValPro 111
QQ	250 GATCACTAI	::: TTACAGTGGAATGT	::::: GTCAGAATATCCAGGG	
δλ	112 ProHisArg	LeuTrpLysProAsi	pValLeuMetTyrAsn	ProHisArgLeuTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAsp 131
qq	310 GATGGCCAG	::::::	CATTCTTCTCTATAAC	GATGGCCAGATTTGGAAACCAGACATTCTTCTATAACAGTGCTGATGAGCGCTTTGAC 369
δλ	132 SerThrTyr	ProThrAsnValVa	lvalArgAsnAsnGly	SerThrTyrProThrAsnValValValArgAsnAsnGlySerCysLeuTyrValProPro 151
Dp	370 GCCACATTC	CACACTAACGTGTT	GGTGAATTCTTCTGGG	GCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGGCATTGCCAGTACCTGCCTCCA 429
67	152 GlyIlePhe	LysSerThrCysLy	sileAspileThrTrp	GlyllePheLysSerThrCysLysIleAsplleThrTrpPheProPheAspAspGlnArg 171
qq	430 GGCATATT	AAGAGTTCCTGCTA	CATCGATGTACGCTGG	STITCCCTTIGATGTGCAGCAC 489
δλ	172 CysGluMet	LyspheGlySerTr	pThrTyrAspGlyTyr	CysGluMetLysPheGlySerTrpThrTyrAspGlyTyrGlnLeuAspLeuGlnLeuGln 191
qq	490 TGCAAACTG	SAAGTTTGGGTCCTG	GTCTTACGGAGGCTGG	TGCAAACTGAAGTTTGGGTCCTGGTCTTACGGAGGCTGGTCCTTGGATGCAGATGCAG 549
δ	192 AspGluGly	GlyGlyAspileSe	rSerPheValThrAsn	AspGluGlyGlyGlyAspIleSerSerPheValThrAsnGlyGluTrpGluLeuIleGly 211
Db	550 GAG	GCAGATATCAG	TGGCTATATCCCCAAT	GGAGAATGGGACCTAGTGGGA 600
Qy	212 ValProGly	VLysArgAsnGlull	eTyrTyrAsnCysCys	ValProGlyLysArgAsnGluIleTyrTyrAsnCysCysProGluProTyrIleAspIle 231
qq	601 ATCCCCGG	Caagaggagtgaaag	GTTCTATGAGTGCTGC	arcccegcaagaggagagggrictargagrigcrecaaagagccracccaargre 660
č	232 ThrPheAl	aValValileArgAr	gLysThrLeuTyrTyr :::	
QQ	661 ACCTICAC	agrgaccargcgccc	cassacscreractar	ACCTTCACAGTGACCATGGGCGGCAGGACGCTCTACTATGGCCTCAACCTGCTGATCCCC 720

252 CysvalleulleAlaSerMethAlateuleuGlyPherhrieuProProAspSerGlyGiu 721 INGGRICHTEACTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	VA466 A A A A A A A A A A A A A A A A A A
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δ d à q ò g $\stackrel{>}{\circ}$ q à d

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This sequence encodes the V247T variant of human alpha7 nicotinic acetylcholine receptor (nAchR) subunit of the invention. Cells containing the DNA are used to express the protein and to identify modulators of alpha7 nAchR activity or cytoprotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating neurogeneration, enzyme dysfunction, affective disorders and immune dysfunction, such as cancer, post-herpetic neuralgia, diabetic convergence as cancer, post-herpetic neuralgia, diabetic convergathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru, cypychocais and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while emonolonal antibodies are used to detect the protein for diagnosis (in vitro or by in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAchR, the protein has about 100-fold greater sensitivity to cholinersein conceptor agonists (nicotine or acetylcholine) and response to these
                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding variant of human alpha 7 nicotinic acetyl-choline receptor sub-unit - used to identify modulators of the receptor, potentially useful for treating neuro-degeneration, cancer etc.
                                                                                                                                                                                                                                                                                                              Gopalakrishnan M, Mckenna DG, Monteggia LM, Roch J;
Touma E;
                                                                    Location/Qualifiers
9. .1517
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Fig 2; 44pp; English.
                                                                                                                                                                                                            97WO-US023405.
                                                                                                                                                                                                                                             96US-00771737
                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-377593/32.
                                                                                                                                                                                                                                                                           (ABBO ) ABBOTT LAB.
   schizophrenia; ss.
                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW69216.
                                                                                                                                                                                                                                                                                                              Briggs CA, G
Sullivan JP,
                                                                                                                                                                                                                                           20-DEC-1996;
                                  Homo sapiens
                                                                                                                                     WO9828331-A2
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                                                                    Key
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> Sequence 1590 BP; 322 A; 471 C; 449 G; 348 T; 0 U; 0 Other; 1590 239 86 127 70 6 Length:
> Matches:
> Conservative:
> Mismatches:
> Indels:
> Gaps: 1.23e-114 1242.00 62.26% 45.79% 46.60% Alignment Scores: Pred. No.: Score:

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:

US-09-303	-232-4 (1	US-09-303-232-4 (1-496) x AAV44687 (1-1590)
δλ	12 AlaP	12 AlaProAlaGlyLeuLeuLeuLeuLeuCysLeuLeuTrpProArgGlyAlaArgCysGly 31
Db	18 AGCC	
δλ	32 TyrH	32 TyrHisGluLysArgLeuLeuHisHisLeuLeuAspHisTyrAsnValLeuGluArgPro 51
Ωþ	78 GAGT	78 GAGTICCAGAGGAAGCITIACAAGGAGCIGGICGAAGAACTACAAICCCIIGGAGAGGCCC 137
QY	52 Valv	52 ValValAsnGluSerAspProLeuGlnLeuSerPheGlyLeuThrLeuMetGlnIleIle 71
Db	138 GTGG	
δ	72 Aspv	72 AspValAspGluLysAsnGlnLeuLeuIleThrAsnIleTrpLeuLysLeuGluTrpAsn 91

198 92 258 112	GACGTGGATGAGAACCAAGTTTTAACCACCAACATTTGGCTGCAAATGTCTTGGACA 257 ASPMELASDLeuArgTrpAsnThrSerAspPheGlyGlyValLysAspLeuArgValPro 111
318 318 132 378	SetThrTyrProThrAshValleuwGeTyrAshSetAlaAspGluGlyPheAsp 131 GATGGCAGATTTGGAAACCAGACATTCTTCTATAACAGTGCTGATGAGGCTTTGAC 377 SetThrTyrProThrAshValValValArgAshAshGlySetCysLeuTyrValProPro 151 ::: :: GCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGGCATTGCCAGTACTGCCTCCA 437
152 438 172 498	GlyllepheLysSerThrCysLysIleaspileThrTrpPhebroPheAspAspGlnarg 17.
192 558	AspGluGlyGlyGlyAspIleSerSerPheValThrAsnGlyGluTrpGluLeuIleGly 211 :::
212	ValProGlyLysArgAsnGlulleTyrTyrAsnCysCysProGluBroTyrIleAsplle 231 :::
232	ThrPheAlaValValIleArgArgLysThrLeuTyrTyrPhePheAsnLeuIleValPro 251
252	CysValLeuIleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGlu 271
272	LysLeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAla 291 ::: :::
292	GluThrMetProAlaThrSerAspAlaValProLeuLeuGlyThrTyrPheAsnCysIle 311
312	MetPheMetValAlaSerSerValValSerThrIleLeuIleLeuAsnTyrHisHisArg 331
332	HisAlaAspThrHisGluMetSerAspTrpIleArgCysValPheLeuTyrTrpLeuPro 351
352	TrpValLeuArgMetSerargProGly360 GGTTCCTGCGAATGAAGAGGCCGGGGAGGACAAGGTGCGCCCGGCCTGCCAGCACAAG 1088
361	SeralaThrThrProProAlaArg 369 CAGCGGCGCTGCAGCTGCCGGCCGCGCGCCGCCGCCGCCGCCGCCGCCGCCGC
370	
373	ProProAspLeuGluLeuArgGluArgSerSerLysSerLeuLeuAlaAsnValLeuAsp 392
393	IleAspAspAspAspPheArgHisProGlnAlaGlnGlnProGlnCysCysArgTyrTyrArg 412 :: GATGAGGACCTCCTGCA
	GAIGAGCACCICCIGCAC

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GlyllephelysserThrCysLyslleAsplleThrTrpPheProPheAspAspGlnArg 171
                                                                                                                                                                                                                                  SerThrTyrProThrAsnValValValArgAsnAsnGlySerCysLeuTyrValProPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetPheMetValAlaSerSerValValSerThrIleLeuIleLeuAsnTyrHisHisArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CysValLeuIleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspGluGlyGlyGlyAspIleSerSerPheValThrAsnGlyGluTrpGluLeuIleGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 ValProGlyLysArgAsnGlulleTyrTyrAsnCysCysProGluProTyrIleAspIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thr Phe AlaValValIle Arg Arg LysThr LeuTyr Tyr Phe Phe Asn LeuIle Val Pro
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                                                                                                                                                                                 GCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGGCATTGCCAGTACCTGCCTCCA
                                                                      12 AlaProAlaGlyLeuLeuLeuLeuCysLeuLeuTrpProArgGlyAlaArgCysGly
                                                                                      TyrHisGluLysArgLeuLeuHisHisLeuLeuAspHisTyrAsnValLeuGluArgPro
                                                                                                                                                                                                                                                                   AspMetAsnLeuArgTrpAsnThrSerAspPheGlyGlyValLysAspLeuArgValPro
                                                                                                                                                                                                                                                                                                                  ProHisArgLeuTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAsp
Mismatches:
            Indels:
                                               (1-1509)
                                                US-09-303-232-4 (1-496) x AAC90385
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                                                                                                                                                                         Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
                                                              452
                                                                                                            472
                                                                                                                                                             492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the coding sequence for a mutant human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells. The protein encoded by this sequence has the wild-type threonine residue at position 230 substituted by a proline
            GlyGlyGluGluAsnGlyAlaGlyLeuAlaAlaHisSerCysPheGlyValAspTyrGlu
                                                                            473 IleIlePheThrLeuPheThrIleIleAlaThrLeuAlaValLeuLeuSerAlaProHis
                                      -GACCCGGAC
                                                                                                               453 AspAlaAspIleSerArgAspTrpLysPheAlaAlaMetValValAspArgLeuCysLeu
                                                              LeuSerLeuIleLeuLysGluIleArgValIleThrAspGlnMetArgLysAspAspGlu
                                                                                                                                                                                                                                                                                                                                                                                 Human; alpha7 nicotinic acetylcholine gated ion channel; mutant; 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
                                                                                                                                                                                                                                                                                                                                                           Mutant human alpha7 ligand gated ion channel coding sequence #1.
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239
86
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Matches:
Conservative:
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                                      1275 égégégeaacececeaagege-
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P-PSDB; AAB50015.
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Score: Percent Similarity:

360	1080	369	1140	372	1200	392	1248	412	1266	432	1296	452	1356	472	1416	492	1476			
	. TGGTTCCTGCGAATGAAGAGGCCCGGGGAGGACAAGGTGCGCCCGGCCTGCCAGCACAAG 108	SerAlaThrThrProProAlaArg	1081 CAGCGCGCTGCAGCCTGGCCAGTGTGGAGATGAGCGCCGTGGCGCCGCCGCCGCCCGC	ValProPro	1141 AACGGGAACCTGCTGTACATCGGCTTCCGCGGCCTGGACGGCGTGCACTGTGTCCCGACC			IleAspAspAspPheArgHisProGlnAlaGlnGlnProGlnCysCysArgTyrTyrArg	GATGAGCACCTCCTGCAC	GlyGlyGluGluAsnGlyAlaGlyLeuAlaAlaHisSerCysPheGlyValAspTyrGlu	1267 GGCGGGCAACCCCCCGAGGGGGACCCGGAC		TIGGCCAAGATCCTGGAAGGTCCGCTACATTGCCAATCGCTTCCGCTGCCAGGACGAA	AspAlaAspIleSerArgAspTrpLysPheAlaAlaMetValValAspArgLeuCysLeu	1357 AGCGAGGCGGTCTGCAGCGAGTGGAAGTTCGCCGCCTGTGTGGTGGACCGCCTGTGCCTC	llellePheThrLeuPheThrilelleAlaThrLeuAlaValLeuLeuSerAlaProHis	ATGGCCTTCTCGGTCTTCACCATCATCACCACCATCGGCATCCTGATGTCGGCTCCCCAAC	IleMet 494	::: 1477 TTCGTG 1482	
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Search completed: May 8, 2004, 19:30:17 Job time : 553.982 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                Copyright
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- protein search, using sw model OM protein

May Run on:

7, 2004, 11:31:03 ; Search time 12.0702 Seconds (without alignments) 3952.801 Million cell updates/sec

US-09-303-232-4 Perfect score:

2665 1 MGGRARRSHLAAPAGLLLLL.....LFTIIATLAVLLSAPHIMVS Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

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Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

alpha 7 neuronal n nicotinic acetylch nicotinic acetylch nicotinic receptor alpha-bungarotoxin nicotinic acetylch hypothetical prote hypothetical prote hypothetical prote nicotinic acetylch Description SUMMARIES JN0113 G02259 ACHUA7 AS7175 AD11378 JH01378 JH01378 S68588 T25671 T19622 T19622 T19622 S12359 A53956 A37040 A40110 S60589 A24572 ACFFA2 ACCHAN ACCHNN ACCH4N JH0174 T09289 S10505 ACFFA1 50548 Query Match Length DB 1267 1242 1241 1241 1232.5 1219.5 1121 1160 1065 Score 979 962 955 954 953 936 936 936 918 908 908 903 903 903 903 902 902 900.5 899 898.5 Result No.

ACRYA1 B37014

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~	Н	7	N	1	7	~	~	N	2	N	7	~	Н	0	N
495	457	500	457	457	470	445	457	517	459	627	457	468	521	625	565
33.7	33.6	33.5	33.4	33.4	33.3	33.3	33.2	33.2	33.2	33.0	32.9	32.9	32.8	32.8	32.6
868	896.5	892.5	890	889	888	887	886	886	885.5	879.5	876.5	875.5	875	874	869
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 JN0113
	nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken N'Alternate names: alpha-bungarotoxin-binding protein alpha chain C.Species: Gallus Gallus (Aricken)
	C;Date: 12-Feb-1993 #sequence revision 12-Feb-1993 #text_change 20-Aug-1999 C;Accession: JN0113; JH0172; \$28018; B25738; S26566 R;Couturier, S; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.;
	A.Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmental. A;Reference number: JN0113; MUID:91097796; PMID:1702646 A;Accession: JN0113 A;Accession: JN0113 A;Accession: DNA
	A, Residues: 1-502 < COUS. A/Cross-references: GBX.K68586; NID:g287756; PIDN:CAA48576.1; PID:g287757 A, Experimental source: white leghorn; brain R, Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
	Arities Erain alpha-bungarotoxin binding protein CDNAs and MAbs reveal subtypes of this Areference number: JH0172; MUID:90315158; PMID:2369519 Areference number: JH0172 Areference number: JH0172 Areference number: JH0172
	A;residues: 1-502 <sch3 1-502="" <sch3="" a;experimental="" a;residues:="" a;resterences:="" ballivet,="" brain="" embl:x52295;="" hernandez,="" j.m.<="" l.;="" m.;="" m.c.;="" matter,="" nid:g63077;="" pid:g63078="" pidn:caa36543.1;="" r;matter-sadzinski,="" roztocil,="" source:="" t.;="" td=""></sch3>
	A:Title: Neuronal specificity of the alpha? nicotinic acetylcholine receptor promoter de A;Reference number: 828018; MUID:93049204; PMID:1425587 A;Accession: 828018 A;Molecule type: DNA
	A; Kestdues: 1-18 cMAS. A; Kestdues: 1-18 cMAS. A; Cross-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320 A; Experimental source: white leghorn; erythrocyte R; Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.; Ra Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985 A; Title: Brain and muscle nicotinic acetylcholine receptors are different but homologous A; Reference number: A94055; MUID:85270494; PMID:3860855
	.43-45, X', 47 <con ceptor is blocked (2; 144/1; 200/1; eptor ion channel; neux status predicted < ylcholine receptor #status predicted #status predicted #status predicted</con
-	F;4/0-488/Domain: transmembrane #status predicted <tr4></tr4>

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F,46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted F;365,367,413,427,465/Binding site: phosphate (Ser) (covalent) #status predicted F;442/Binding site: phosphate (Thr) (covalent) #status predicted F;442/Binding site: phosphate (Thr) (covalent) #status predicted
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C.Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-Aug-1999
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                                                                                                                                                                                                                                                   E----DKVRPACQHKQRRCSLSSMEMNTVSGQQCSNGNMLYIGFRGLDGVHCTPTTDS
                                                                                                                                                      1 MGGRARRSHLAAPAGILLLLCLLMPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ
                                                                                                                                                                               LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA
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                                                                                      Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change
C;Accession: G02259
R;Leonard, S.
submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                      47.5%; Score 1267; DB 2; Length 5
48.6%; Pred. No. 1.7e-102;
live 83; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha 7 neuronal nicotinic acetylcholine receptor - human
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46.0%; Pred. No. 2.6e-100;
tive 84; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Reference number: H00936
A,Accession: G02259
A,Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-502 <LEO>
                                                                                                        Best Local Similarity
Matches 249; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S:
Matches 240
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nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human N;Alternate names: cholinergic nicotinate receptor alpha-7 chain C;Species: Homo sapiens [man] C;Species: Homo sapiens [man] C;Date: 12-Aug-1996 #sequence revision 31-Jan-1997 #text_change 22-Jun-1999 C;Accession: I37185; A54194; $60309 Miller, V; Anand, R; Lindstrom, J. Mol. Pharmacol. 45, 546-554, 1994 A;Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               omers expressed in Xenopus Occytes.

A;Reference number: 137185; MUID:94195283; PMID:8145738
A;Accession: 137185
A;Accession: 137185
A;Accession: 137185
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-502 <PEN3.
A;Residues: 1-502 <PEN3.
A;Cross-references: EMBL:X70297; NID:g496606; PIDN:CAA49778.1; PID:g496607
A;Cross-references: brain neuroblastoma cell line SHSY-5Y
B;Chini, B; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heinemann, S.
B;Chini, B, 2381, 1994
A;Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotinic
A;Reference number: A54194; MUID:94245214; PMID:8188270
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A;Cross-references: GDB:138751; OMIM:118511
A;Map position: 15q14-15q14
C;Complex: the functional receptor molecule is a heteropentamer with two alpha chains c;Complex: the functional receptor molecule is a heteropentamer; ion channel; neurotransmitter receptor F;1-23/Domain: signal sequence #status predicted <SGS>F;2-50/Domain: transmembrane #status predicted <TR1>F;2-2-280/Domain: transmembrane #status predicted <TR2>F;2-6-217/Domain: transmembrane #status predicted <TR2>F;2-6-317/Domain: transmembrane #status predicted <TR3>F;40-488/Domain: transmembrane #status predicted <TR3>F;40-498/Domain: transmembrane #status predicted <TR3>F;40-490/J33/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Molecule type: mRNA
A;Residues: 24-363,'S',365-374,'A',376-408,'AWPAP',414-502 <CHI>A;Cross-references: GB:Z23141; NID:g457736; PIDN:CAA80672.1; PID:g457737
A;Experimental source: retina
C;Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and
                                      B---ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTWRRRTLYYGLNLLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                          DEGGGDISSFVINGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP
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Cispeciaes: T01379
Risequela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
J. Neurosci. 13, 596-604, 1993
A;Thle: Molecular cloning, functional properties, and distribution of rat base and A;Reference number: Z14310; MUID:93147931; PMID:7678857
A;Reference number: Z14310; MUID:93147931; PMID:7678857
A;Reference number: Z14310; MUID:93147931; PMID:368857
A;Reference number: Z14310; MUID:93147931; PMID:368857
A;Residues: 1-502 <8EGA
A;Residues: 1-502 <8EGA
A;Cross-references: EMBL:553987; NID:9264770; PIDN:AABE55224.2; PID:95705903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 VYFSLSLLQIMDVDEKNQVLTTNIWLQMSWTDHYLQWNMSEYPGVKNYRFFDGGIWKPDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GGR------GGIWLALAAALLHVSLQGEFQRRLYXELVKNYNPLERPVANDSQPLTV
                                                                                                                                             1 MGGRARRSHLAAPAGLILLILCLILWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ
                                                                                                                                                                                                1 MCGRRGGIWLALAAALLHV-----SLOGEFORRLYKELVKNYNPLERPVANDSOPLT
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                                         Length 502,
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                                    Query Match
46.6%; Score 1241; DB 2;
Best Local Similarity 47.1%; Pred. No. 3.2e-100;
Matches 243; Conservative 90; Mismatches 139;
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47.2%; Pred. No. 1.8e-
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Matches 244; Conservative
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A; Residues: 1-502 cORP>
A; Cross-references: GB.L137663; NID:g790853; PIDN:AAC42053.1; PID:g790854
C; Superfamily: acetylcholine receptor
C; Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;
F; L23/Domain: signal sequence #status predicted <SIG>
F; 24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted or Signal sequence #status predicted <TR1>
F; 262-280/Domain: transmembrane #status predicted <TR2>
F; 26-317/Domain: transmembrane #status predicted <TR3>
F; 46,90,133/Binding site: arbohydrate (Asn) (covalent) #status predicted
F; 365,413,427/Binding site: phosphate (Thr) (covalent) #status predicted
F; 441/Binding site: phosphate (Tyr) (covalent) #status predicted
F; 442/Binding site: phosphate (Tyr) (covalent) #status predicted
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C;Species: Mus musculus (house mouse)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
C;Accession: A57175
B;Ort-Urtrager, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.
A;Title: Cloning and mapping of the mouse alpha7-neuronal nicotinic acetylcholine adjacession: A57175; MUID:95324936; PMID:7601470
A;Status: preliminary
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F,150-164/Disulfide bonds: #status predicted
F;365,413/Binding site: phosphate (Ser) (covalent) #status predicted
F;415/Binding site: phosphate (Thr) (covalent) #status predicted
F;442/Binding site: phosphate (Tyr) (covalent) #status predicted
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Pred. No. 3.2e-100;
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                                                                                                                                     46.6%;
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Db 193ADISNYISNGEWDLVGVPGKRNELYYECCKEPYPDVTYTITMRRRTLYYGLNLLIPC 249 Qy 253 VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVPLNWVAETMPATSDAVPLLGTYFNCIM 312 250 VLISGLALLVFLLPADSGEKISLGTTVLISLTVFMLLVAEIMPATSDSVPLIGYFASIM 309 Qy 313 FMVASGVVSTILLINYHHRADTHEMSDWIRCVFLYMLPWVLEMSRPGSATTPPPARVPP 372 "	RESULT 7 568586 nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 06-Dec-1996 #eequence_revision 07-Feb-1997 #text_change 20-Aug-1999 C;Accession: S68588; S57496 R;Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D. J. Mol. Biol. 258, 261-269, 1996 A;Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans. A;Reference number: S68587; MUID:96196478; PMID:8627624 A;Accession: S68588 A;Status: mucleic acid sequence not shown A;Residues: 1-498 https://document.new.nchance A;Coss-references: EMBL:X83887; NID:g872087; PIDN:CAA58764.1; PID:g872088 C;Superfamily: acetylcholine receptor C;Reywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane F;10-19/Domain: signal sequence #status predicted <sig> F;20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <mat< th=""><th> Query Match 45.1%; Score 1201; DB 2; Length 498; Best Local Similarity 46.0%; Pred. No. 9.9e-97; Matches 230; Conservative 89; Mismatches 151; Indels 30; Gaps 7; </th><th> 137 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDBGGGG</th><th>Db 185 DISEYISNGEWALPLITVERNEKFYDCCPEPYPDVHFYLHMRRRTLYYGFNLIMPCILIT 244 Qy 257 SMALLGFTLPPDSGEKLSLGVTILLSLIVFLNMVAETMPATSDAVPLLGTYFNCIMFMVA 316 [</th></mat<></sig>	Query Match 45.1%; Score 1201; DB 2; Length 498; Best Local Similarity 46.0%; Pred. No. 9.9e-97; Matches 230; Conservative 89; Mismatches 151; Indels 30; Gaps 7;	137 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDBGGGG	Db 185 DISEYISNGEWALPLITVERNEKFYDCCPEPYPDVHFYLHMRRRTLYYGFNLIMPCILIT 244 Qy 257 SMALLGFTLPPDSGEKLSLGVTILLSLIVFLNMVAETMPATSDAVPLLGTYFNCIMFMVA 316 [
	ACVUDELCLIFTLETITATIAVLESAPHIM 494		45.8%; Score 1219.5; DB 2; Length 511; similarity 46.3%; Pred. No. 2.5e-98; conservative 88; Mismatches 131; Indels 55; Gaps LCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIID	14 LC-LWASLFLSFFKVSQQGESQRRLYRDLLRNYNRLERPUMNDSQPIVVELQISLLQIID 72 73 VDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDS 132 73 VDEKNQVLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDS 132 73 VDEKNQVLITNAMLQMYWVDIXLSWDQYEYPGVQNLRPFSDQIWVPDILLYNSADERPDA 132 133 TYPTNVVVRNGSCLXVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYSGYQLDLQLQD 192 134 TYPTNVLVNYRSGSCQXIPPGIFKSTCKIDITWFPFDVQKCDLKFGSWTHSGWLIDLQMLE 192 135 TFHTNVLVNYSGSCQXIPPGIFKSTCXIDVRWFPFDVQKCDLKFGSWTHSGWLIDLQMLE 192 195 EGGGDISSFVTNGEWELLGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVVC 252 197 EGGGDISSFVTNGEWELLGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVVC 252

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Query Match
Best Local S:
Matches 217
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                                                                                                                                                                                                   hypothetical protein D2092.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T2571
R;Gattung, S.; Maggi, L.
Submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid D2092.
A;Reference number: Z20067
A;Accession: T2571
A;Accession: T2571
A;Accession: T2571
A;Accession: T461
A;Accession: T461
A;Accession: EMBL:U88167; PIDN:AAB42223.1; GSPDB:GN00019; CESP:D2092.3
A;Experimental source: strain Bristol N2; clone D2092
C;Genetics:
A;Gene: CESP:D2092.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 DAGEKITLEVIILLAIVFFLSMVSEMTPPTSEAVPLIGVFFSCCMLVVSASVVFTIVVLN 325
                                                 18 ISSNGTTTDVSQQATLLILHRIYHELKIVTKRMIEGDKEEQACNNWKFAAMVVDRLCLYV 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---YEAQILLLHSVHTELRR 408
----NRHSESLIRNIKDNEHSLSRANSFDADCRINQYIMTQSVSNGLTSLGSIPSTM 417
                            HSCFGVDYELS----LIL----KEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLII 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILN 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---YKFVK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGG----DISSFVTNGEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 NIRWNTSDFGGVKDLRVP--PHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 EKRLIHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 1
A;Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1141; DB 2;
Pred. No. 1.5e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 LHFRSADSHEMNPLVRRVLLEFLPWLLFMSRPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 ANVIDSTDKM-PKKPKNPLDCNL----PSNHAG
                                                                                             FTLFTIIATLAVLLSAPHIM 494
                                                                                                              ||:| |::|::
FTIFIIVSTIGIFWSAPYLV 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.8%;
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Best Local Similarity 46.2
Matches 218; Conservative
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T19622 hypothetical protein C31H5.3 - Caenorhabditis elegans

RESULT

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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T19622
R;Kershaw, J: 19622
R;Kershaw, J: 1963
R;Reference number: 219153
R;Reference number: 219153
R;Reference number: 219153
R;Residues: 1560
R;Kesidues: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19862
R;Hembry, C.
Submitted to the EMBL Data Library, March 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 ILLILICLINPRGARC-----GYHEKRLIHHILDHYNVLERPVVNESDPLQLSFGLTLMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 IIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 FDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 FDSTWPVNAVVLYTGNVTWIPPAIIRSSCAIDIAYFPFDTGHCTWKFGSWTYSGFFTDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 LQDEGGGDISSFVT-----NGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.8%; Score 1060; DB 2; ilarity 37.6%; Pred. No. 2.4e-84; Conservative 96; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RERSSKSLLANV
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11;

10;

Gaps

78;

#status predicted

20 63

183 188

242

303

357 401

ANVLDIDDDFRHPQ

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sequence of the mature human nicotinic acetylcholine receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 -----RV---PEQLLADLASKRLLRHAHNSKLSAAAAAAAAAASSSAASSPDSLRHHH 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Aug-1999
C;Accession: A55956; 821338
R;Mihovilovic, M.; Roses, D.
Bxp. Neurol. 111, 175-180, 1991
A;Title: Expression of mRNAs in human thymus coding for the alpha3 subunit cA;Reference number: A53956; MUID:91114756; PMID:1989896
                                                                                                                                                                                                                                                                                                                                          64 IDLNLKDQILTTNVWLEHEWQDHKFRWDPAEYGGVTELYVPSEHIWLPDIVLYNNADGEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469 PFELEKATHNVLFIQNHAQRQDEFDAE-DQDWGFVAMVLDRLFLWIFTIASIVGTFAILC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 VVITMIKAVLHHIGKVVWIPPALFKSSCEIDVRYFPFDQQICFMKFGSWIYDGDQIDLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AAPAGLLILLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQI
                                                                                                                                                                                                                                      4 ALPPMILILILILILIHHPAAANPDAKRLYDDILSNYNRLIRPVSNNTDTVLVKLGIRLSQL
                                                                                                                                                                                                                                                                                                             71 IDVDEKNOLLITINIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGF
                                                                                                                                                                                                                                                                                                                                                                                                                            131 DSTYPTNVVVRINGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --QLQDEG----GGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 LHQHQHHLQLHHLQRPGGCNGLHSATNRFGGSAGAFGGLPSVVGLDGSLSDVATRKKY
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-503 < MIH>
A, Cross-references: GB: M37981; NID: g189252; PIDN: AAA59942.1; PID: g189253
R, Anand, R.; Lindstrom, J.
submitted to the EMBL Data Library, June 1990
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A;Molecule type: mRNA
A;Residues: 30-503 <ANA>
A;Cross-references: BMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C;Genetics:
                                                                                 ; Score 979; DB 2; Length 55; Pred. No. 2.8e-77; 88; Mismatches 160; Indels
  F;501-523/Domain: transmembrane #status predicted <TM
F;47,235/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 AQQPQCCRY----YRGGEENGAGLAAH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 TTPPPARVPPPDLELRERSSKSLL
                                                                                    36.7%;
                                                                                                                                            Conservative
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A,Reference number: S21338
                                                                                                               Similarity
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                                                                              Query Match
Best Local Simi:
Matches 217;
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C;Species: Schistocerca gregaria (desert locust)
C;Species: Schistocerca gregaria (desert locust)
C;Species: 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: 512359
C;Accession: 612359
C;Acce
                                                                                                                                                                                                                              9
                                                                                                                                                                                     A,Map position: X
A,Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1;
C,Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 VVSTILLILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG------SATTPPPA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITD 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRVTYSKVMAESYVEDVVMTELNKYMQ------KACL---ELKNISSQTRAMRK 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---PQAQQ 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89
                                                 A;Residues: 1-542 <WIL>
A;Cross-references: EMBL:Z70266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 GEWNLLAVPARHETNIFD--EQPYPSLFFYLIIQRRTLYYGLNLIIPSFLISLMTVLGFT
                                                                                                                                                                                                                                                                                                                                                                                                                      EKRLIHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIRWNTSDFGGVKDIRVP--PHRIWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ-----DEGGGDISSFVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFT
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 542;
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                                                                                                                                                                                                                                                                                                       39.6%; Score 1055.5; DB 2;
40.5%; Pred. No. 5.6e-84;
tive 94; Mismatches 136;
preliminary; translated from GB/EMBL/DDBJ
                                                                                                A; Experimental source: clone C40C9
C; Genetics:
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 40.5%
Matches 214; Conservative
                                                                                                                                                             A, Gene: CESP: C40C9.2
                             A; Molecule type: DNA
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430

----SCFGVD----

527

the alpha3 subunit of a neuronal

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F;240-264/Domain: transmembrane #status predicted <TMl>F;272-290/Domain: transmembrane #status predicted <TM2>
36.0%;
39.2%;
Query Match
Best Local Similarity 39.2%
Matches 198; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 3R 96A
A; Introns: 64/3; 79/3;
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C;bacte: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C;Accession: 800377
R;Nef, P.; Oneyser, C.; Alliod, C.; Couturier, S.; Ballivet, M.
A;Title: Genes expressed in the brain define three distinct neuronal nicotinic acetylchd A;Reference number: 800376; MUID:88283624; PMID:3267226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Superfamily: acetylcholine receptor
C.Superfamily: acetylcholine receptor
C.Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-52/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <MAT>
F;24-250/Domain: transmembrane #status predicted <TM1>
F;305-327/Domain: transmembrane #status predicted <TM3>
F;502-520/Domain: transmembrane #status predicted <TM4>
F;502-520/Domain: transmembrane #status predicted <TM4>
F;54,104/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;158-172,222-223/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                   245
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                                                                                                                                                                                                                                                                                                     126 ADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQ 185
                                                                                                                                                                                                                                                                                                                                                                                     125 AVGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYFPFDYQNCTMKFGSWSYDKAK 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 TYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRP----GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTPPPARVPPPDLELRERS-SKSLLANVLDIDDDFRHPQAQQPQC--CRYYRGGEEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 AOKPRPLYGAELSNINCFSRAESKGCKEG-----YP-CODGMCGYCHHRRIKISNF
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A;Residues: 1-528 <NEF>
A;Cross-references: EMBL:X07339; NID:g62792; PIDN:CAB59645.1; PID:g6136914
C;Genetics:
A;Introns: 21/1; 73/3; 88/3; 125/2; 487/3
                                                                                                                                                                                           10 LAAPAG----LLLLL.CLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGL
                                                                                                                                                                                                                               LAAPGAVAPRLLLLLLSLLP-VARASEAEHRLFERLFEDYNEIIRPVANVSDPVIIHFEV
                                                                                                                                                 Gaps
                                                                                                                                                 34;
                                                                                                     Length 503;
                                                                                                                                                 89; Mismatches 172; Indels
                                                                                                     Score 962; DB 2;
Pred. No. 7.3e-76;
      A;Cross-references: GDB:125219; OMIM:118503
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                                            A,Map position: 15q24-15q24
C,Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 GAGLA-AHSCFGVDYELSL
                                                                                                          36.1%;
                                                                                                                             41.1%;
                                                                                                                                                      206; Conservative
                                                                                                       Query Match
Best Local Similarity
Matches 206; Conserv
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A; Introns: 64/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3
C; Superfamily: acetylcholine receptor
C; Superfamily: acetylcholine receptor
C; Reywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-567/Product: nicotinic acetylcholine receptor alpha-like chain #status predicted <}
F;22-240/pomain: extracellular #status predicted <EXT>
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                                                                                                                                                                                                          NDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVP
                                                                                                                                                                                                                                                           SDYKLRWNPEDFDNVTSIRVPSEMIWIPDIVLYNNADGEFAVTHWTKAHLFSNGKVKWVP
                                                                                                                                                                                                                                                                                                             151 PGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGGDISSFVTNGEWELL
                                                                                                                                                                                                                                                                                                                                           211 GVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                              210 NAIGRYNSKKYDCCTEIYPDITFYFVIRRLPLFYTINLIIPCLLISCLTVLVFYLPSDCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- PPPDLELRERS
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                                                                                                        GYHEKRILLHHILDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEW
                                                        Gaps
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A/Molecule type: DNA
A/Residues: 1-567 < BOS>
A/Cross-references: GB:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A/Accession: A38801
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Residues: 1-567 < BOZ>
A/Cross-references: EMBL:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
                                                        62;
     Length 528;
; Score 959; DB 1; Length 52; Pred. No. 1.4e-75; 84; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Conservation of neural nicotinic acetylcholine A,Reference number: S00381; MUID:88283626; PMID:2840281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 RHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP
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A;Cross-references: FlyBase:FBgn0000036
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C;Keywords: neurotransmitter receptor; transmembrane protein
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-502/Product: nicotinic acetylcholine receptor alpha-3 chain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CjAccession: A37040; S24595
R) Fornasari, D.; Chini, B.; Tarroni, P.; Clementi, F.
R) Fornasari, D.; Chini, B.; Tarroni, P.; Clementi, F.
R) Fornasari, D.; Chini, B.; Tarroni, P.; Clementi, F.
R) Fornasari, D.; Chini, B.; Tarroni, P.; Clementi, F.
R) Fornasari, D.; Chini, B.; Tarroni, P.; Clementi, F.
R) Fornasion and the control of human neuronal nicotinic receptor alpha-3-subunit.
A; Reference number: A37040, MUID:90245296; PMID:2336208
A; Residues: 1-502 «FOR»
A; Residues: 1-502 «FOR»
A; Residues: 1-502 «FOR»
A; Coss-references: EMBL:X52239; NID:9177897; PIDN:AAC84176.1; PID:9177898
C; Superfamily: acetylcholine receptor
C; Keywords: neurotransmitter receptor; transmembrane protein
F; 1-28/Domain: signal sequence #status predicted <SIG>
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C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 VPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFN 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 CIMFMVASSVVSTILLILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPPAR 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 ANVLDI---DDDFRHPQAQ----QPQCCRYYRGGEENGAGLAAHS----CFGVDY--ELS 434
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                                                                                                                                                                                                                                                                                         QLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTN
                                                                                                                                                                                                                                                                                                                                                                     138 VVVRNNGSCLYVPPGIFKSTCKIDITWFFFDDQRCEMKFGSWTYDGYQLDL----QLQD-
                                                                                                                                                                                                                                                                                                                                                                                               18 LLLCLIMPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKN
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40.8%; Pred. No. 3.6e-75;
Live 90; Mismatches 174; Indels 30;
                                                                                                                           Length 567;
                                                                                                                                                                    Indels
               F;326-513/Domain: intracellular #status predicted <INT>
F;514-523/Domain: transmembrane #status predicted <TM4>
F;45,233/Binding site: carbohydrate (Asn) (covalent) #status
F;149-163,222-223/Disulfide bonds: #status predicted
;306-325/Domain: transmembrane #status predicted <TM3>
                                                                                                                       Score 957.5; DB 1;
Pred. No. 2.1e-75;
5; Mismatches 174;
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38.2%; Pred
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Best Local Similarity 40.8%
Marches 203; Conservative
                                                                                                                                          Best_Local Similarity 38.2%
Matches 206; Conservative
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IIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEG 129
                                                                                                       VPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFN 309
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                                                                               FDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQ
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Search completed: May 7, 2004, 11:39:31 Job time : 13.0702 secs Ч

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 7, 2004, 11:18:28 ; Search time 9.26316 Seconds (without alignments) 2788.120 Million cell updates/sec

Title: Perfect score:

US-09-303-232-4
2665
1 MGGRARRSHLAAPAGLLLLL.....LFTIIATLAVLLSAPHINVS 496 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	P22770 qallus qall	1 homo sa	2 mus n	11 ratt	P54131 bos taurus	caen	99	P23414 schistocerc	P32297 homo sapien	homo	0 gallu	_		Q07263 bos taurus	~			homo sa	qallu	P09484 gallus gall	torpedo			homo	rattu	P02710 torpedo cal	in	0		m	25	8 rattus no	90
SUMMARIES		ID	CHIC	ACH7 HUMAN	ACH7 MOUSE	ACH7_RAT		ACH1_CAEEL		ACH1 SCHGR			- 1		ACH2_RAT	ACH3 BOVIN	ACH3_RAT	ACH2_DROME	ACHA CHICK	ACH6_HUMAN	ACH3 CHICK	ACHN_CHICK	ACHA_TORMA	ACH4_CHICK	ACHP HUMAN		ACHP_RAT	- 1	ACH3_CARAU	ACHN RAT	ACHA BOVIN	ACH6 RAT	ACH4 DROME	ACHA RAT	ACHA_MOUSE
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ACHP_CHICK ACH6_CHICK ACH0_CARAU ACHA_BRARE ACH4_HUMAN ACH2_XENLA ACH2_XENLA ACH8_CAEEL ACH8_CAEEL ACH4_RAT ACH4_RAT ACH4_RAT ACH4_RAT ACH4_RAT ACH4_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 Mutations in the channel domain alter desensitization of a neuronal
                                                                                                                                                          FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: Alpha-7 transcripts transiently accumulate in the developing optic tectum between E5 and E16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

L-S<sub>2</sub> T: SUPPRESESE INHIBITION BY THE

OPEN-CHANNEL BLOCKER QX-222.
                                                     MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC. MEDLINE=93024917; PubMed=1383829; Galzi J.-L., Devillers-Thiery A., Hussy N., Bertrand S., Changeux J.-P., Bertrand D.; "Mutations in the channel domain of a neuronal nicotinic receptor convert ion selectivity from cationic to anionic."; Nature 359:500-505(1992).
                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                           membrane.
SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.5%; Score 1267; DB 1; Length 502;
48.6%; Pred. No. 8.9e-99;
Live 83; Mismatches 144; Indels 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family; 3D-structure.
                                                                                                                                                                                                                                     bungarotoxin. The structure is probably pentameric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           572325D4309AD2FD CRC64;
                                                                                                                                                                                                                                                         SIMILALLY).
SUBCELLULAR LOCATION: Integral membrane protein.
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EXTRACELLULAR
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InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur channel.
Pfam; PF02931; Neur chan LBD; 1.
Pfam; PF02932; Neur chan memb; 1.
PRINTS; PR00252; NRIONCHĀNNEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGROOBEO; LIC;
                nicotinic receptor.";
Nature 353:846-849(1991).
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164
213
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PDB; 1KC4; 17-APR-02.
PDB; 1KL8; 17-APR-02.
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502 AA;
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Gaps

36;

1 MGGRARRSHLAAPAGLLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ

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<u>:</u> = -

249; Conservative

Local

Matches

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300
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                                                                   IDDDFRHPQAQQ 404
-----RESLQGEFQRKLYKELLKNYNPLERPVANDSQPLT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94195283; PubMed=8145738;
Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;
Peng X., Kxys W., Gerzanich V., Anand R., Lindstrom J.;
From the SH-Sysy cell line and determination of pharmacological
properties of native receptors and functional alpha 7 homomers
expressed in Xenopus oocytes.";
                                                                                                                                                 290 VPLIAQYFASTMIIVGLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLINWCAWFLRMKRPG
                                                                                                                                                                                                           YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK
                                                                                                                                                                                                                                                                                           TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA
                                                                                                                                                                                                                                                                                                                 : | | : | | | : | | | E-----DKVRPACQHKQRRCSLSSMEMNTVSGQQCSNGNMLYIGFRGLDGVHCTPTTDS
                                                                                                                         LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POCCRYYRGG--EENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97062879; PubMed=8906617; Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A., Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A., Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A., Harpold M.M.; Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.; 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits ", 1.217-228(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACH7_HUMAN STANDARD; PRT; 502 AA.
195644; 015826; 096RH2; 099555; 09RXH0;
01-UNN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
8-FPB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
CHRNA7 OR NACHRA7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463 AAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 SATTPPPARVPPPPDLELRERSSKSLLANVLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Pharmacol. 45:546-554(1994).
  MGLRALMLWLLAAAGLV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Hippocampus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [3]
SEQUENCE FROM N.A.
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TISSUE=Breast cancer;
MEDLINE=21829512; PubMed=11840567;
                                                                                                                                  TISSUE=Retina;
MEDLINE=94245214; PubMed=8188270;
                                                                                                                     Drug Dev. Res. 30:252-256(1993).
                                                                   TISSUE=Epidermal keratinocytes;
                                    FEBS Lett. 400:309-314(1997)
                                                                                         SEQUENCE OF 17-502 FROM N.A.
                                                                                                                             SEQUENCE OF 24-502 FROM N.A.
                                                                                                                                                         nicotinic receptor subunit
Genomics 19:379-381(1994).
     SEQUENCE FROM N.A.
                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                      SPECTROMETRY
                                                                                                                                                Heinemann S.F.;
                                                                                              TISSUE-Brain;
                                                                                                                                                                                                                                                           membrane.
                                                                                                                 receptor."
                                             REVISIONS
                                                  Groot
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192 DEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 APAGLILLICLLWPRGARCGYHEKRLLHHILDHYNVLERPVVNESDPLOLSFGLTLMQII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 DVDERNQVLTTNIMLQMSWIDHYLQMNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BÝ SIMILARITY.
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
ALPHA-7 CHAIN.
                                                                                                                                                                                                                              R GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan...;
R GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan...;
R GO; GO:0015464; F:acetylcholine receptor activity; TAS.
R GO; GO:001879; F:nicotinic acetylcholine-activated cation-se...;
R GO; GO:0000810; F:ransport; TAS.
R GO; GO:0006810; P:transport; TAS.
R InterPro; IPR006629; Neu channel memb.
R InterPro; IPR006202; Neur channel.
R EnterPro; IPR006201; Neur channel.
R Ffam; PF02931; Neur chan EBD; 1.
R Ffam; PF02932; Neur chan memb; 1.
R FRIMTS; PR00252; Neur chan memb; 1.
R R RIGRFAMS; TIGRO866; LIC; 1.
R PROSITE; ES00236; NEUROTE ION CHANNEL; 1.
R PROSITE; ES00236; NEUROTE ION CHANNEL; 1.
R PROSITE; ES00236; NEUROTE ION CHANNEL; 1.
R PROSITE: FROMENER ION CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.

BY SIMILARITY.

ASSOCIATED WITH RECEPTOR ACTIVATION

(BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 A -> G (IN REF. 1 AND 7).
58 S -> N (IN REF. 2 AND 6).
134 C -> S (IN REF. 2 AND 6).
364 C -> S (IN REF. 8).
375 A -> G (IN REF. 8).
373 A -> G (IN REF. 10).
56449 MW; D94B3A482EAAOB42 CRC64;
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", U40583; AAA83561.1; -.
") U6436; AAB40114.1; -.
") Y08420; CAA6967.1; -.
") AF38558; AAK68111.1; -.
") L2827; -; NOT ANOTATED_CDS.
") Z23141; CAA80672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Multigene family.
                                                                                                                              EMBL; AF332758; AAK19515'1;
PIR; G02259; G02259.
PIR; 137185; ACHUA7.
                                                                                                                                                                                                HGNC:1960; CHRNA7.
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                                        EMBL;
EMBL;
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                        MEDLINE=97162233; PubMed=9009220; Groot Kormelink P.J., Luyten W.H.M.L.; Groot Kormelink P.J., Luyten W.H.M.L.; Cloning and sequence of full-length CONAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SYSY and/or IMR-32.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 118-129 FROM N.A.
MEDLINE=21818878; PubMed=11829490;
Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
A. 3-Mb map of a large segmental duplication overlapping the alpha7-
nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
Genomics 79:197-209(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: After binding acetylcholine, the ACMR responds by an extensive change in conformation that affects all submits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning and chromosomal localization of the human alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T., Lee J., Tian J., Glordano T., "Cloning and sequence of the human a7 nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A., Zvelebil M.J., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J., "Cluster analysis of an extensive human breast cancer cell line protein expression map database.";

Proteomics 2:212-223(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
MASS SPECTROMETRY: NW=54157.68; METHOD=MALDI.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretti M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Forms a homo-oligomeric channel blocked by alphabungarotoxin. The structure is probably pentameric (By
                                                                                                                                                                                                                                                                                                                               Arredondo J., Grando S.A., "Cloning cholinergic receptors in human keratinocytes.", Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                             Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subunit gene (CHRNA7).";
                                                                                                                                                                                                                         Kormelink P.J., Luyten W.H.M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X70297; CAA49778.1; -.
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9

70; Gaps

502;

DB 1; Length

131

63 71

191

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POTENTIAL
                                                                                                                                                            46 N-
90 N-
133 N-
56631 MW;
                                                                                                                                                                                                                                                               46.6%;
                                                                                                                                                                                                                                                                                Local Similarity 47.1
nes 243; Conservative
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                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                    392
                                                                                                                          416
                                                                                                                                                                  452
                                                                                                                                                                                                          452
                             | :| ||| ||:::| |||| | :| | | :| | 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 360 || 36
                                                                                    VPPPPDLELRERSSKSLLANVLD
                                                                                                                                                                                          ANOSILL,
POSTISYNAPTIC membrane; Lour.
Postsynaptic membrane; Multigene family.
1 22 BY SIMILARITY.
1 22 BY SIMILARITY.
1 CONTROL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                      361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTH----
                                                                                                                                                                  393 IDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 26:399-402(1995).
-!-PUNCITION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sumlidarity/).
SUBCELLULIAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Forms a homo-oligomeric channel blocked by alphabungarotoxin. The structure is probably pentameric (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BALB/c; TISSUE=Brain; MEDLINE=95324936; PubMed=7601470; Orr-Urtreger A., Seldin M.F., Baldini A., Beaudet A.L.; "Cloning and mapping of the mouse alpha 7-neuronal nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
      MEMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG-
                                                                                                                                                                                                                                                   453 DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                        SEAVCSEWKFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPHA-7 CHAIN.
EXTRACELLULAR (POTENTIAL)
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MGD; MGI:99779; Chrna7.

InterPro; IPR006029; Neu channel memb InterPro; IPR006020; Neur chan LBD.

InterPro; IPR006201; Neur chan LBD.

Pfam; PF02931; Neur chan LBD; 1.

Pfam; PF02932; Neur chan LBD; 1.

PRINTS; PR00252; NRIGNGHANEL.

TIGREAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                               -----SATTPPPAR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acetylcholine receptor.";
                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
                                                                                                                                                                                                                 -DEHLLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDGYQLDLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGGWSLDLQMQE---ADISSYIPNGEWDLMGIPGKRNEKFYECCKEPYPDVTYTVTMRRR 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPLLGTYFNCIMFNVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 EDKVRPACQHKP------RRCSLASV-ELSAGAGPPTSNGNLLYIGFRGLEGNHCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---ENGAGLAAHSCFGV------DYELSLILKEIRVITDOMRKDDEDADISR
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MCGRRGGIWLALAAALLHV-----SLOGEFORRLYKELVKNYNPLERPVANDSQPLT
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=93147931; PubMed=7678857; Sequela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.; "Molecular cloning, functional properties, and distribution of rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ol-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
CHRNA7 OR ACRA7.
Bukattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SATTPPPARVPPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGE-
                                                POTENTIAL.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).
                                                                                                                                        (BY SIMILARITY).
N-LINKED (GECNAC. . .) (POTENTIAL)
N-LINKED (GECNAC. . .) (POTENTIAL)
N-LINKED (GECNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                 Length 502;
                                                                                                                                                                                                                                                                               ; Score 1241; DB 1; Length 5; Pred. No. 1.4e-96; 90; Mismatches 139; Indels
                                                                                                                                                                                                                                    C9312E5226D120E3 CRC64;
POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :||||| ||||||||: |::|||| |: :
EWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
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361
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            54 YFSLSLLQIMDVDEKNQVLTTNIWLQMSWTDHYLQWNMSEYPGVKNVRFPDGQIWKPDIL 113
                                                                                                                                                                                                                 LYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAV 301
                                                                                                                                                                                                                                                                                                                                                                             351 DKVRPACQHKPRRCSLASVELSAGAGPPTSN------GNLLYI--GFRGLEGMHCA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 PTPDSGVVCGRLACSPTHDEHLMHGAHPSDG-DPDLAKILEBVRYIANRNRCQDESEVIC 457
                                                                            182 DGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKT
                                                                                                                                                                                                                                                                                                 PLLGTYFNCIMFMVASSVVSTILLILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              400 PQAQQPQCCRYYRGGEENGAGL--AAHSCFGVDYELSLILKEIRVITDQMRKDDEDADIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Forms a homo-oligomeric channel blocked by alphabungarotoxin. The structure is probably pentameric (By similarity). Homo-oligomer of the short form gives rise to unfunctional channels, as does coexpression of both long and short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95346009; PubMed=7620615;
Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.,
Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.,
Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.,
Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.,
Alpha-Bungarotoxin-sensitive nicotinic receptors on bovine
chromaffin cells: molecular cloning, functional expression and
alternative splicing of the alpha 7 subunit.",
Furction: After binding acceptionine, the AChR responds by an
extensive change in conformation that affects all subunits and
leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOId=P54131-2; Sequence=VSP 000075;
TISSUE SPECIFICITY: At least in chromaffin cells.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458 RDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A. (ISOFORMS LONG AND SHORT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       499 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOVIN
                                                                                                                                                                                                                                                                                                 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACH7_BOV
P54131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHRNA7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 SFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGRARRSHLAAPAGLLILILCLLWPRGARCGYHEKRLLHHILDHYNVLERPVVNESDPLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                   Hartley M.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1998) to check actylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                        similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                        by alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 502;
alpha 7: a nicotinic cation channel highly permeable to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEURONAL ACETYLCHOLINE RECEPTOR
ALPHA-7 CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Postsynaptic membrane; Ionic Channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Forms a homo-oligomeric channel blocked by albungarotoxin. The structure is probably pentameric (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 141; Indels
                                                                                                                                   Bounce, 0.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       00996E74EC7B9A56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
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N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
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-> R (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1232.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, L31619; AAC33136.1; -...
PIR; T01379; T01378
InterPro; IPR006020; Neu channel memblinterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur chan LBD.
Pfam; PP02931; Neur chan LBD; 1.
Pfam; PP02932; Neur chan LBD; 1.
PRINTS; PR00222; NEUCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
                                                                                                     STRAIN=Sprague-Dawley; TISSUE=Brain;
                                                                                                                                                                                                        STRAIN=Sprague-Dawley; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Postsynaptic memorane; Multigene family.
Transmembrane; Multigene family.
22 BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
                                        Neurosci. 13:596-604(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56410 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S53987; AAB25224.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 AA;
                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                 REVISION TO 363.
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TRANSMEM
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                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIDDDFRHPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVITDQMRKDD 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 VDEKNQVLTTINIWLQMTWTDHYLQMNASEYPGVKTVRFPDGQIWKPDILLYNSADERFDA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RGSLCLALAASILHVSLQGEFQRKLYKDLVKNYNPLERPVANDSLPLTVYFSLSLLQIMD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIID 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ADISGYIPNGEWDLVGVLGKRSEKFYECCKEPYPDVTFTVSIRRTLYYGLNLLIPC
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NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
Missing (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                     DR InterPro; IPR006029; Neu channel memb.
DR InterPro; IPR006202; Neur channel memb.
DR InterPro; IPR006202; Neur channel.
DR InterPro; IPR006201; Neur channel.
DR Ffam; PF02931; Neur chan memb; 1.
DR PRIMY; PF02932; NRIONCHANNEL.
DR TIGROBGO; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
DR PROSITE; PR00236; NEUROTR ION CHANNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.7%; Score 1218.5; DB 1; Length 499;
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80; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALPHA-7 CHAIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEE5D0B3820D42D5 CRC64;
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BY SIMILAR
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--DPDLAKILEEVRYIAHRFRCQD 448
                                                                                                                                                                                                                                         Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Nelson J., Wohldmann P., Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
- FUNCTION: Possible acetylcholine receptor.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                  STRAIN=Bristol N2;

Bablines 26196478; PubMed=8627624;
Ballivet M., Alliod C., Bertrand S., Bertrand D.;
"Nicotinic acetylcholine receptors in the nematode Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor like protein, alpha-type chain precursor.
F25G6.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL)
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Pfam, PR02931; Neur_chan_LBD; 1.
Pfam, PR02932; Neur chan memb, 1.
PRINTS; PR00252; NRTONCHANNEL.
TIGRRAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
                          EDADISRDWKFAAMVVDRLCLIFTLFTIATLAVLLSAPHIM 494
                                                        491
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EXTRACELLULAR (POTENTIAL)
                                           CYTOPLASMIC (POTENTIAL) POTENTIAL.
                                                                                                                              498 AA
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InterPro; IPR006029; Neu_channel_me:
InterPro; IPR006202; Neur_chan_LBD.
                                                                                                                                                                                                                                                                                                                                                                           elegans.";
J. Mol. Biol. 258:261-269(1996).
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  412 THDEHLLH--AGQP--
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P48180;
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NQLLITNIWLKLEMNDMNLRMNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPT 136
                                                                                                                                                                                                                                                  NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGG 196
                                                                                                                                                                                                    DISSFVTINGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIA 256
                                                                                                                                                                                                                                                                                                                                       SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVA 316
                                                                                                                                                                                                                                                                                                                                                                                                       SSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGS----ATTPPPARVPP 372
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WA MEDLINE-98424077; PubMed-9753155;
WA Eartham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Towner P.,
A Reynolds S.E., Wolstenholme A.J., Wonnacott S.;
Reynolds S.E., Wolstenholme A.J., Wonnacott S.;
R. "Characterization of a nicotinic acetylcholine receptor from the RT insect Manduca sexta.";
L. "Characterization of a nicotinic acetylcholine receptor from the RT insect manduca sexta.";
L. "Insect Manduca sexta.";
C. -- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma membrane (By similarity).
C. -- SUBCELDULAR LOCATION: Integral membrane protein.
C. -- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
                                                                                                                                       17 LLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEK
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                                                                                     Gaps
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01-NoV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-like chain precursor (MARA1)
93 N-LINKED (GLCNAC. . .) (POTENTIAL)
57169 MW; E463ABB40AC9FA82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQC-CRYYRGGEENGAGLAA-
                                                      Length 498;
                                               45.1%; Score 1201; DB 1; Length 4 46.0%; Pred. No. 3.1e-93; Live 89; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 AA.
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FTIFIIVSTIGIFWSAPYLV 497
                                                                                 Matches 230; Conservative
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 93
498 AA;
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P91766;
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Pfam; PF02932; Neur chan memb; 1.
PF13932; Neur chan memb; 1.
PRINTS, PR00252; NRTCONCHANNEL.
PTGREAMS; TIGRO0866; LIC; 1.
PROSITE; PS00236; NEUROTR ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
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LIKE CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.5%; Pred. No. 1.1e-/%;
tive 75; Mismatches 159; Indels
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                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.8%; Score 980.5; DB 1
40.5%; Pred. No. 1.1e-74;
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                                                                                                           EMBL; Y09795; CAA70928.1; -.
InterPro; IPR006029; Neu channel memb.
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur channel.
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Transmembrane; Multigene family
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516 AA;
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--ANVLDIDDDFRHPQ 401

RESULT

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P23414

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-YELSLILKEIRVITDQMRKDDE-DADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLL 488
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                                                                                                                          64 IDLNLKDQILTTNVWLEHEWQDHKFRWDPAEYGGVTELYVPSEHIWLPDIVLYNNADGEY 123
                                                                                                                                                                                                         124 VVTTMTKAVLHHTGKVVWTPPA1FKSSCEIDVRYFPFDQQTCFMKFGSWTYDGDQIDLKH 183
                                                                                                                                                                                                                                                                                                                                                     YYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVP 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 LHOHOHHLOLHHLORPGGCNGLHSATNRFGGSAGAFGGLPSVVGLDGSLSDVATRKKY 468
                                       4 ALPPMLILILILILIHPAAANPDAKRLYDDILSNYNRLIRPVSNNTDTVLVKLGLRLSQL
                                                                                                                                                                                                                                                                                          71 IDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGF
                                                                                                                                                                                   131 DSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDL--
                                                                                                                                                                                                                                                                    --QLQDEG----GGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRKTL
               11 AAPAGLILILICILWPRGARCGYHEKRILHHILIDHYNVLERPVVNESDPLOLSFGLTLMQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mihovilovic M., Roses A.D.;
"Expression of mRNMs in human thymus coding for the alpha 3 subunit of a neuronal acetylcholine receptor.";
Exp. Neurol. 111:175-180(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P32297; Q15823; Q96KH3; Q99553; Q9BQ93; Q1-0CT-1993 (Rel. 27, Created) C1-0CT-1997 (Rel. 35, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Neuronal acetylcholine receptor protein, alpha-3 chain precursor. CHRNA3 OR NACHRA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDILINE=9024526; PubMed=2336208;
FORDARAT D., Chini B., Tarroni P., Clementi F.;
"Molecular cloning of human neuronal nicotinic receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 TTPPPARVPPPDLELRERSSKSLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            402 AOOPOCCRY----YRGGEENGAGLAAH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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MEDLINE=91114756; PubMed=1989896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [3]
SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=97062879; PubMed=8906617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurosci. Lett. 111:351-356(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
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InterPro; IPR006029; Neur channel memb.
InterPro; IPR006202; Neur channel.
InterPro; IPR006201; Neur channel.
Pfam; PF02931; Neur chan memb; 1.
Pfam; PF02922; Neur chan memb; 1.
PRINTS; PR00252; NEUROCHĀNNEL.
TIGRFAMS; TIGR00860; LIC; I.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91092263; PubMed=1702381;
Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,
Darlison M.G., Sattelle D.B., Barnard B.A.;
Darlison M.G., Sattelle D.B., Barnard B.A.;
Darlison M.G., Sattelle D.B., Barnard B.A.;
Esquence and functional expression of a single alpha subunit of an insect nicotinic acetylcholine receptor.";
EMBO J. 9:4391-4398(1990).
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
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                                                                                                                                                                                                                                                                      Eukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.7%; Score 979; DB 1; Length 557; 40.0%; Pred. No. 1.6e-74; ive 88; Mismatches 160; Indels '
                                                                                                                                                                    01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-Li chain precursor.
Schistocerca gregaria (Desert locust).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168389C887DFDF3E CRC64;
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                            557 AA
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|:|| | |||| :: :: | || || 462 VLDRPFLWIFTLAVVVGSAGIILQAP 487
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SIGNAL 1 23 PO
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                                                                                                                              STANDARD;
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165
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Matches 217; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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DOMAIN TRANSMEM TRANSMEM TRANSMEM DOMAIN

CHAIN

TRANSMEM DISULFID DISULFID

CARBOHYD DOMAIN

DOMAIN

CARBOHYD

Query Match SEQUENCE

Event=Alternative splicing; Named isoforms=2;

Name=1; Isold=P32297-1; Sequence=Displayed;

Q

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worlby K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Ahlting M., Madan A., Young A.C., Shovchenko Y., Bouffard G.G.,
Anting M., Madan A., Young A.C., Shovchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Ghenerth A., Schein J.E., Jones S.J.M., Marra M.A.,
Human and mouse CDNA sequences."
Human and mouse CDNA sequences."
Human and mouse CDNA sequences."
                                                                                                                                                                                                                                                                                                                                             [5]
SEQUENCE FROM N.A. (ISOFORM 2).
SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=99118870; PubMed=9921897;
Rempel N., Heyers S., Engels H., Sleegers E., Steinlein O.K.;
"The structures of the human neuronal nicotinic acetylcholine receptor beta2- and alpha3-subunit genes (CHRNB2 and CHRNR3).";
Hum. Genet. 103:645-653(1998).
                                                                                                                                                                                           MEDLINE=97162233; PubMed=9009220;
Groot Kormelink P.J., Luyten W.H.M.L.;
"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAchR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32.";
FEBS Lett. 400:309-314(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND VARIANT LEU-21 INS.
MEDLINE=21342809; PubMed=11450844;
Lev-Lehman B., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.;
"Characterization of the human beta4 nAChR gene and polymorphisms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Epidermal keratinocytes;
Arredondo J., Grando S.A.;
"Cloning cholineggic receptors in human keratinocytes.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all submits and leads to opening of an ion-conducting channel across the plasma
Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
"Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anand R., Lindstrom J.;
Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                          beta 4 subunits.";
J. Mol. Neurosci. 7:217-228(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Hum. Genet. 46:362-366(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1)
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-!- SUBUNIT: Neuronal AChR seems to be composed of two different type of subunits: alpha and non-alpha (betA).
-!- SUBCELLUIAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:

membrane.

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                                               Note=No experimental confirmation available; SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSLPLALSP<sup>-</sup>-> ALAAPGAVA (IN REF. 2).

LSPP -> CRA (IN REF. 1).

D -> G (IN REF. 1).

DD -> TT (IN REF. 1).

I -> S (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MALAV -> MGSGPL (in isoform 2).

/FIId=VSP_000073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALPHA-3 CHAIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
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                                      IsoId=P32297-2; Sequence=VSP 000073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                                         EMBL; AUG07783; CAA07682.1; --
EMBL; AJ007783; CAA07682.1; --
EMBL; AJ007784; CAA07682.1; JOINED.
EMBL; AJ007785; CAA07682.1; JOINED.
EMBL; AJ007785; CAA07682.1; JOINED.
EMBL; AJ007787; CAA07682.1; JOINED.
EMBL; BC001642; AH01642.1; --
EMBL; BC002996; AAH01642.1; --
EMBL; RC002396; AAH01642.1; --
EMBL; AF38584; AAK68110.1; --
EMBL; AF38589; CAA37625.1; --
PIR; A37040; A37040.
                                                                                                                                                                           U62432; AAB40110.1; -.
Y08418; CAA69695.1; -.
                                                                                                                                                       EMBL; M86383; AAC84176.1; -.
EMBL; M37981; AAA59942.1; -.
                                                                                                                                                                                                                                                                                                                   Genew; HGNC:1957; CHRNA3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 VDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYFPFDYQNCTWKFGSWSYDKAKIDLVVI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSSSSSVDAVLSLSALSPEIKEAIQSVKYIAENMKAQNEAKEIQDDWKYVAMVIDRIFLW 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ 191
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                                                                                                                                                                                                                  12 APAGLILLICLLWPRGARCGYHEKRLLHHILDHYNVLERPVVNESDPLQLSFGLTLMQII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 MFMVASSVVSTILIILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRP----GSATTPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 MIFVTLSIVITVEVLNVHYRTPTTHTMPSWVKTVFLNLLPRVMFMTRPTSNEGNAQKPRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor
CHRNA2.
                                                                                                                                                       30;
                                                                                       Length 503;
                                                                                    36.0%; Score 960; DB 1; Length 50 llarity 41.0%; Pred. No. 5.6e-73; Conservative 90; Mismatches 172; Indels
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SEQUENCE FROM N.A.
Groot Kormelink P.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
L -> V (IN REF. 1).
RA9EBC5D71AEC7D6 CRC64;
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MEDLINE=97062879; PubMed=8906617;
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Neurosci. 7:217-228(1996)
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                             57309 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474 IFTLFTIIATLAVLL 488
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   430
503 AA;
                                                                                                                       Similarity
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .; TAS
                                                                                                                                                                        SUBUNIT: Neuronal AChR seems to be composed of two different types of subunits: alpha and non-alpha (beta). Alpha-2 subunit can be combined to beta-2 or beta-4 to give rise to functional receptors. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 RARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-2 CHAIN.
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Dischart From N.T. Rosenthal A.;
Submitted (OCT-2000) to the BMBL/GenBank/DDBJ databases.
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R Genew; HGNC:1956; CHRRAZ:

R MIM; 118502; -

R QG: QG: OG05892; CINICOTINIC acetylcholine-gated receptor-chan...;

GG: QG: OG05892; CINICOTINIC acetylcholine-gated receptor-chan...;

GG: QG: OG01564; F: acetylcholine receptor activity; TAS.

GG: QG: OG01565; F: signal transduction; TAS.

GG: QG: OG07165; P: signal transduction; TAS.

R GG: GG: OG07268; P: synaptic transduction; TAS.

R InterPro; IPR006602; Neur_channel.memb.

R InterPro; IPR006201; Neur_channel.memb.

R Pf002931; Neur_chan_memb; 1.

R Pf102932; Neur_chan_memb; 1.

R PROSITE; PS00236; NEINCHANNEL.

R PROSITE; PS00236; NEURORFAINEL; 1.

R PROSITE; PS00236; NEURORFAINEL; 1.

R PROSITE; PS00236; NEURORFAINEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
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**LINKED (GLCNAC. . .) (POTENTIAL)

**N-LINKED (GLCNAC. . .) (POTENTIAL)

**N-LINKED (GLCNAC. . .) (POTENTIAL)
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EMBL, Y16281, CAA76154.1; -.
EMBL, AF311103; -, NOT_ANNOTATED_CDS.
Genew, HONC:1956; CHRNA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane, Multigene family
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                                                                                                                                                                                                                                                                                                                                                                398
                                                                                                                                                                                                                                                                                                                                                                                                  384 -PPVELCHP--LRIKLSPSYHWLESNVDAEEREVVVEEEDRWACAGHVAPSVGTLCSHG 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 HLHSGASGPKAEALLQEGE---LLLSPH------MQKALEGVHYIADHLRSEDADSSV 489
149 NNADGEFAVTHMTKAHLFSTGTVHWVPPAIYKSSCSIDVTFFPFDQQNCKMKFGSWTYDK 208
                                                 184 YQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLY 243
                                                                                                                                                   YFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVARTMPATSDAVPL 303
                                                                                                                                                                                TINLIIPCLLISCLTVLVFYLPSDCGEKITLCISVLLSLTVFLLLITEIIPSTSLVIPL 327
                                                                                                                                                                                                                                                       LGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSAT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                         --HPQAQQPQCCRYYRGGEENGAGLAAHSCFGVDYELSLILKEIRVIIDQMRKDDEDADI 456
                                                                                              209 AKIDLE-OMEQTVDLKDYWESGEWAIVNATGTYNSKKYDCCAEIYPDVTYAFVIRRLPLF
                                                                                                                                                                                                                                                                                                      328 IGEYLLFTMIFVTLSIVITVFVLNVHHRSPSTHTMPHWVRGALLGCVPRWLLMNRP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae, Gallus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nef P., Oneyser C., Alliod C., Couturier S., Ballivet M.;
"Genes expressed in the brain define three distinct neuronal
nicotinic acetylcholine receptors.";
EMBO J. 7:555-601 (1988).
-!- FUNCTION: After binding acetylcholine, the AChR responds by an
extensive change in conformation that affects all subunits and
leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane.
-!- SUBUNIT: Neuronal AChR seems to be composed of two different type of subunits: alpha and non-alpha (also called beta). A functional receptor seems to consist of two alpha-chains and three non-alpha chains.
-!- SUBCELUTIAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FBB-2003 (Rel. 4), Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
                                                                                                                                                                                                                                                                                                                                                        364 TPPPARVPPPDLELRERSSKSLLANVLD-----IDDDFR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           457 SRDWKFAAMVVDRLCLIIFTLFTIIATLAVLL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        490 KEDWKYVAMVIDRIFLWLFIIVCFLGTIGLFL 521
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EMBL; X07341; CABS9645.1; JOINED.
EMBL; X07342; CABS9645.1; JOINED.
EMBL; X07343; CABS9645.1; JOINED.
EMBL; X07344; CABS9645.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHICK
                                                                                                                                                                                                     268
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ID ACH2 CH
DT ACH2 CH
DT 01-MARN
DT 01-MARN
DT 08-FBB
DE Neurory
OC Burdary
OC Burdary
OC Archos
OC Gallus
OC Gallus
OC Gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP------PPPDLELRERS 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 NDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 PGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGGDISSFVTNGEWELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 GVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSG
                                                                                                                                                                                                                                            NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-2 CHAIN.
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 SRCWLET--DVDDKWEEEEEEEEEEEEEEKAYPSRVPSGGSQ---GTQCHYSCERQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---ILKEIRVITDOMRKDDEDADISRDWKFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 RSPSTHTMPHWVRSFFLGFIPRWLFMKR-----PPLLLPAEGTTGQYDPPGTRL
                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
PIR; S00377; ACCHAN.

InterPro; IPR006029; Neu channel memb.
InterPro; IPR006202; Neur channel.
InterPro; IPR006202; Neur channel.
Pfam; PF02931; Neur chan memb; 1.
Pfam; PF02932; Neur chan memb; 1.
PRINTS; PR00252; NEICONCHANNEL.
ITGREAMS; TIGR0086; LIC; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
POSTSYDADLIC membrane; Ionic channel; Glycoprotein; Signal; Iransmembrane; Multigene family.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E76C6360AF876364 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 959; DB 1;
Pred. No. 7.2e-73;
                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60675 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 39.21
Matches 198; Conservative
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172
223
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104
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272
306
328
502
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104
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ID ACH1_DROME
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                                                                                                                                                                                                                                                                                                                                                                             RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Bashburner M., Henderson S.N.,
Sutron G.G., Norders Y.-H.C., Blazej R.G., Chang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfeiffer B.D.,
RA Batla M.A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Bescon K.Y., Benco P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Buuck J., Bardstardin D., Blolshakov S.,
Borkova D., Botchan M.R., Buuck J., Bandari D., Bolshakov S.,
Burtis R.C., Busem D.A., Buller H., Cadieu E., Center A., Chadra I.,
RA Burtis R.C., Busem D.A., Buller G., Bavengort L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dagan-Rocha S., Dunkov B.C., Dunn P.
RA Dodson K., Doup L.E., Downes M., Dagan-Rocha S., Dunkov B.C., Dunn P.
RA Dodson K., Doup L.E., Downes M., Dagan-Rocha S., Dunkov B.C.,
Britis N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Gennison J.A., Retchum K.A.,
Alali M., Kalush F., Karpen G.H., Kez Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Kez Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Kez Z., Kennison J.A., Ketchum K.A.,
Alali M., Murphy B., Murphy L., Muzhy D.M., Nelson D.L.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., McBherson D.,
Rendert K., Nelson K.A., Nixon K., Nixon M., Nelson D.L.,
Rajer E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Wang Z.-Y., Wassarman D.A., Weinster E., Wang A., Wang Z.-Y., Wassarman D.A., Weinster E., Wang G., Zhao G., Zh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Bernan B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richker J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                   Bossy B., Ballivet M., Spierer P.; "Conservation of neural nicotinic acetylcholine receptors from Drosophila to vertebrate central nervous systems."; EMBO J. 7:611-618(1988).
01-MAR-1989 (Rel. 10, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Acetylcholine receptor protein, alpha-like chain 1 precursor.
NACR-ALPHA-96AA OR ACRB OR ALS ON ACR96AA OR CG5610.
                                                                                                                 Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                     Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22426069; PubMed=12537572;
                                                                                                                                                                                                                       STRAIN=Oregon-R;
MEDLINE=88283626; PubMed=2840281;
                                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                          STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lewis S.E.;
                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE 1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 LLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 VFIALHFATGGLANPDAKRLYDDLLSNÝNRLIRÞVGNNSDRLTVKMGLRLSQLIDVNLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 VVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDL---QLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---BGGGDISSFVTNGEWELIGVPCKRNEIYYNCCPEPYIDITFAVVIRKTLYYFFNLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family; Polymorphism.
                                                                                                                                         TISSUE SPECIFICITY: CNS in embryos. DEVELOPMENTAL STAGE: Late embryonic, late pupal and second instar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                   FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-
                                                                                                                                                                                                              SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.9%; Score 956.5; DB 1; Length 567; 38.2%; Pred. No. 1.3e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08E1F721FB2A92AC CRC64;
                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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L -> H (IN REF. 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006029; Neu channel memb.
InterPro; IPR006029; Neur chan LBD.
InterPro; IPR006202; Neur chan LBD.
Pfam; PF02931; Neur chan LBD; 1.
Pfam; PF02932; Neur chan memb; 1.
Pran; PR02925; Neur chan memb; 1.
TIGRPANs; TIGR0860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0000036; nAcR-alpha-96Aa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X07194; CAA30172.1; -. EMBL; AE003747; AAF56301.2; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              567 AA;
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                                                                                                                                                                                          larvae stages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
272
306
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VARIANT
CONFLICT
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TRANSMEM
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                                           387
                                                                                                   IPCVGISFLSVLVFYLPSDSGEKISLCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLL 308
                           CIMEMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPAR 369
                                                                                                                                       388 ANVLDI----DDDFRHPQAQ-----QPQCCRYYRGGEENGAGLAAHS-----CFGVDY--ELS 434
                                                                                                                                                                                                  493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Neuronal AChR seems to be composed of two different types of subunits: alpha and non-alpha (beta). Alpha-2 subunit can be combined to beta-2 or beta-4 to give rise to functional receptors. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                  427 PSSLPLPGADDDLFSPSGLNGDISPGCC-----PAAAAAAAADLSPTFEXPYAREME
                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                               LILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boulter J., Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley; TISSUE=Brain; MEDLINE=B8178113; PubMed=2832952; Mada K., Ballivet M., Boulter J., Connolly J.G., Wada E., Mancon L.W., Heinemann S.F., Patrick J.; "Functional expression of a new pharmacological subtype of brain nicotinic acetylcholine receptor.";
                                                                                                                                                                                                                                                                                                511 AA
                                                                                 VPP-----PPDLE-LRERSSKSL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A40110; A40110.
InterPro; IPR006029; Neu_channel_memb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L10077; AAB60900.1; --
EMBL; M20297; AAA40664.1; --
EMBL; M20292; AAA40664.1; JOINED.
EMBL; M20294; AAA40664.1; JOINED.
EMBL; M20294; AAA40664.1; JOINED.
EMBL; M20296; AAA40664.1; JOINED.
EMBL; M20296; AAA40664.1; JOINED.
                                                                                                                                                                                                                                                                                                          P12389; 008952;
01-007-1989 (Rel. 12, Created)
15-UUL-1998 (Rel. 36, Last ann
28-FBB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 240:330-334(1988)
                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane.
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REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLI 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 LKL--SPSYHWLETNMDAGEREETEEEEE-----DENICVCAGL-PDSSMGVLYG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 LLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 ASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 VDLKDYWESGEWALINATGTYNSKKYDCCAEIYPDVTYYFVIRRLPLFYTINLIIPCLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---ELSLILKEIRVITDQMRKDDEDADISRDWKFAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 HGGLHLRAMEPETKTPSQASEIILSPQIQKALEGVHYIADRLRSEDADSSVKEDWKYVAM
                                                                                                                                     NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-2 CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEEN---GAGLAAHSCFGVDY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48; Gaps
                                                                                                                                                                                                                                                                                                BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
InterPro; IPR006201; Neur_channel.
Pfam; PF02931; Neur_chan lbb; 1.
Pfam; PF02932; Neur_chan memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TRGRAPM; TGRORGO, LIC; I.
PROSITE; PS00236; NBTONCHANNEL; 1.
PROSITE; PS00236; NBTONCHANNEL; 1.
PROSITE; PS00246; NBTONCHANNEL; 1.
PROSITE; PR00246; NBTONCHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                 -> S (IN REF. 1; AAA40664).
3824E83BB01D613B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 951; DB 1;
Pred. No. 3.3e-72;
                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     495 AA.
                                                                                                                                                                                                                                                CYTOPLASMIC.
POTENTIAL.
POLY-GLU.
                                                                                                                                                                                                                 POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                   58611 MW;
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Nature 319:368-374(1986).
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InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur channel.
InterPro; IPR006201; Neur channel.
Pfam; PF02931; Neur chan memb; 1.
Pfam; PF02932; Neur chan memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
PRINTS; PR00236; NRIONCHANNEL, 1.
PROSITE; PS00236; NBUROTR ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           composed of two different type
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                                                                                                                                                                                                                                       MEDLINE=92119195; PubMed=1620271;
Criado M., Alamo L., Navarro A.;
Criado M., Alamo L., Navarro A.;
"Primary structure of an agonist binding subunit of the nicotinic acetylcholine receptor from bovine adrenal chromaffin cells.";
Neurochem. Res. 17:281-287(1992).
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Neuronal AChR seems to be composed of two different to subunits: alpha and non-alpha (betA).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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39.5%;
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Matches 198; Conservative
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406 SANLTRSSSSESVDAVLSLSALSPEIKEAIQSVKYIAENMKAQNEAKEIQDDWKYVAMVI 465
                                                                     116 NAVGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYFPFDYQNCTMKFGSWSYDKA 175
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                                                                                                                                                                                                           245 FFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLL 304
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILINE=88041184; PubMed=2444984;
MeDiler J., Connolly J.G., Deneris E.S., Goldman D.J., Heinemann S.F.,
Partick J.;
SADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGY
                                                                                                                                                      QLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYY
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J. Biol. Chem. 269:10252-10264(1994).
-:- FUNCTION. After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last amontation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
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MEDLINE=86118671; PubMed=3753746;
Boulter J., Farns K., Goldman D.J., Martin G., Treco D., Heinemann S.F.,
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SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES OF SUBUNITS: ALEHA AND NON-ALPHA, BETA, ALPHA-3 SUBUNIT CAN BE COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                EMBL; X03440; CAA27170.1; ---
EMBL; X03440; CAA27170.1; ---
EMBL; U4961; AAA41673.1; ---
EMBL; U04961; AAA41601.1; ---
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_channel.
Ffam; PF02931; Neur_chan_memb; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRICONCHANNEL.
IIGREAM'S; TIGR00860; LIC; I.
PROSITE; PS00236; NEUROTR ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
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ALPHA-3 CHAIN.
EXTRACELLULAR.
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N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (PROBABLE).

D66C491E832B9C34 (RC64;
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310

δ СP 369

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414 TRSSSSESVNAVLSLSALSPEIKEAIQSVKYIAENMKAQNVAKEIQDDWKYVAMVIDRIF 473
  --- YP-CQDGTCGYCHHRRVKISNFSANL 413
                                            ------AAHSCFGVDYELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLC 471
364 RIFYGAELSNINCFSRADSKSCKEG----
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Search completed: May 7, 2004, 11:36:32 Job time : 10.2632 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 11:30:03 ; Search time 31.1579 Seconds (without alignments) 5022.709 Million cell updates/sec May Run on:

US-09-303-232-4

1 MGGRARRSHLAAPAGLLILL.......LFTIIATLAVLLSAPHIMVS 496 2665 Perfect score: Sequence:

BLOSUM62 Scoring table: 1017041 segs, 315518202 residues Searched:

Gapop 10.0 , Gapext 0.5

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPIREMBL 25:* Database :

sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
sp_organelle:*
sp_phage:* unclassified: * sp_vertebrate:* sp_rvirus:*
sp_bacteriap:* rodent:* sp_plant:* sp_virus:* 112: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:

SS	Description	O9xxi3 heliothis v	08t7v5 drosophila	O86mn7 drosophila		09xzi4 heliothis v	O8t7s2 drosophila	O8t7s1 drosophila	O86mn8 drosophila	O8t.7s3 drosophila	O8t7s0 drosophila	08t7r9 drosophila	09v179 drosophila	Osipe2 drosophila	O800c7 brachydanio	O7t2u0 fuon rubrin	THE POST OF THE PO
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ALIGNMENTS

01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 24, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Putative nicotinic acetylcholine receptor alpha 7-1 subunit.
Heliothis virescens (Noctuid moth) (Owlet moth).
Eukaryota, Metazoa; Archropoda; Hexapoda; Insecta; Pterygota;
Nocptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Heliothis. InterPro; InterPro; Neur Cnan LBD.

Pfam; PF02931; Neur Channel memb.

Pfam; PF02931; Neur Channel LBD; 1.

Pfam; PF02932; Neur Chan memb; 1.

PRINTS; PR0252; NRIONCHANNEL.

PROSITE; PS00236; NEUROTR ION CHANNEL; 1.

Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Transmembrane. 496 AA. PRT; PRELIMINARY; Q9XZI3 RESULT 1 Q9XZI3 A STATE OF THE STA

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Gaps

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17 LLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          712 QGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDW
R GO; GO:0005216; F:ion channel activity; IEA.

GO; GO:0005216; F:neurotransmitter receptor activity; IEA.

R GO; GO:0006811; P:ion transport; IEA.

R GO; GO:0007268; P:synaptic transmission; IEA.

R InterPro; IPR006201; Neur_channel.

R InterPro; IPR006202; Neur_channel.

R InterPro; IPR006029; Neur_channel.

R Pfam; PF02931; Neur_chan LEB.

R Pfam; PF02931; Neur_chan memb; 1.

R Pfam; PF02932; Neur_chan memb; 1.

R TIGRPAMS; TIGRO0860; LIC; 1.

R PROSITE; PS00256; NEUROTR ION CHANNEL; 1.

R PROSITE; PS00256; NEUROTR ION CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           807;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TrEMBLrel. 25, Last annotation update)
Nicotinic acctylcholine receptor subunit Dalpha7 precursor.
NACRALPA-18C.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                        77.5%; Score 2064.5; DB 5; Length 76.7%; Pred. No. 6.2e-192; ive 32; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                        807 AA; 91223 MW; C8B4F6B34287C8C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIMVS 496
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Best Local Similarity
Matches 396; Conserv
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                                                                                                                                                                                                                                                                                                                                                     Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 YDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                       LSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV 120
                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 SATTPPPARVPPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAG 420
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-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
EMBL; AR712778, AAM13390.1; -.
Flybase; FBGM0028875; nAcR-alpha-34B.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005230; F:extracellular ligand-gated ion channel acti. .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SATTPPPARVPPPDDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCRYYRGGEENGAG
                                                                                                                                                                                                    MGGRARRSHLAAPAGILLILLCLLWPRGARCGYHEKRLLHHILLDHYNVLERPVVNESDPLQ
                                                                                                                                                                                                                                                                                                                  LSFGLTLMQIIDVDEKNQLLITNIWLKCEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDV
                                                                                                                                                                                                                                                                                                                                                                                                                              LMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWT
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                                                                                                                                                                   1 MGGRARRSHLAAPAGLLLLLCLLWPRGARCGYHEKRLLHHLLDHYNVLERPVVNESDPLQ
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MEDLINE=21969411; PubMed=11973307;
MEDLINE=21969411; PubMed=11973307;
MEDLINE=21969411; PubMed=11973307;
Mozauso M., Reenan R.A., Culetto E., Sattelle D.B.;
"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
Genetics 160:1519-1533(2002).
                                                                                                                      Gaps
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalpha5 subunit.
NACR-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 (CG4498 OR CG16878 OR CG32975.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
                                                                                                                   ö
                                                                   Length 496;
                                                                                                                Indels
                56347 MW; 8032FED8515A6210 CRC64;
                                                                Score 2665; DB 5;
Pred. No. 9.4e-251;
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                                                                                                                   0; Mismatches
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                                                                   100.08;
                                                                                           100.08;
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                  496 AA;
                                                                                        Similarity
                                                                                           Best Local Sim:
Matches 496;
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                SEQUENCE
                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 ATTPPPARVPPP-----HPQA- 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 V----GYECPPPPSSSSSASGEKKQQIQNVELKERSSKSLLANVLDIDDDFRCNHRCAS 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDLTFAVVIRRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 GGRM----LVVGLGLLIMI-----PACAAGPHEKRLLHALLDNYNSLERPVVNESDPLQL
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                                                                                                                                                                                                                                                                                                                                                       NICOTINIC ACETYLCHOLINE RECEPTOR SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54;
A Millar N.S.,
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ554210; CAD686936.1; -.
R GO; GO:0016020; C:membrane; ISA.
R GO; GO:0015230; F:extracellular ligand-gated ion channel acti
R GO; GO:00130594; F:extracellular ligand-gated ion channel acti
R GO; GO:00130594; F:neurotransmitter receptor activity; IEA.
R GO; GO:00130594; F:neurotransmitter receptor activity; IEA.
R InterPro; IPR006201; Neur channel.
R InterPro; IPR006202; Neur channel.
R InterPro; IPR006202; Neur chan LBD.
R InterPro; IPR006202; Neur chan LBD.
R Fam; PF02931; Neur chan LBD; 1.
R Fam; PF02932; Neur chan LBD; 1.
R FINTYS, RROSES; NEURCHANNEL; 1.
R FROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Indels
                                                                                                                                                                                                                                                                                                                                                                                          69D2C39746BB74D7 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.8%; Score 2047; DB 5; Best Local Similarity 74.4%; Pred. No. 1.8e-190; Matches 399; Conservative 36; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                          DALPHA7
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                                                                                                                                                                                                                                                                                                                                                                                            542 AA; 60988 MW;
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542
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Drosophila melanogaster (Fruit fly). Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CG32538 protein.
NACR-ALPHA-18C OR CG802 OR CG8109 OR CG32538.
Drosophila melanogaster (Fruit fly)
The melanogaster (Fruit fly)

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RA Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celliker S.E., Holt R.A., Saburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Asburner M., Henderson S.N., RA Faradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Ballew R.M. Basu A., Baxendall D., Shang Q., Chen L.X., Baldwin D., RA Ballew R.M., Basu A., Baxendalle J., Barraktarologu L., Basaley E.M., Ballew R.M., Batu A., Barendari D., Bhandari D., Bolshakov S., Ballew R.M., Bother B.D., Bartham B.P., Handfari D., Bolshakov S., Borkova D., Botham M.R., Bouck J., Bavckstein P., Brottier P., RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies B.M., A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies B.M., A Cherry J.M., Cawley S., Dahlke C., Perraz C., Ferriera S., Dunkov B.C., Dunn P., Bodson K., Doug L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doug L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Brottin D., Houston K.A., Harris M.L., Harryey D., Heiman T.J., Hernandez J.R., Hostin D., Houston K.A., Kalush F., Karpen G.H., Karjen G.H., Wei M.-H., Libegwan C., Laisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Alush F., Karpen G.H., Karvitz S., Kulp D., Lai Z., Mandler B.B., Kodira C.D., Kraft C., Marvitz S., Kulp D., Lai Z., Mandler B.M., Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A., Moshrefi A., Mosh M., Mirchy B., Murphy L., Muzny D.M., Nelson D.L., Rainert K., Pendigon N., Pittman G.S., Pan S., Pollard J., Puri, Y., Wate B.C., Siden-Kiamos I. Simpson M., Strong R., Sun E., Sheng K.H., Zhong F.N., Zaveri J.S., Zhu X., Zhu S., Zhu X., Smith T., Sheng X.H., Zhong F.N., Zhong F.N., Zhang G.Doc, S., Zhu S., Shu B.C., Zaveri J.S.
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Banzon J., An H., Baldwin D., Banzon J., Besandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Blesan D.A.,

Carlson J.W., Center W. Doup L.E., Dayle C., Dresnek D., Farfan D.,

Perriera S., Frise E., Galle R.P., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A begwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Rhouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,

"Sequencing of prosophila melanogaster genome.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Annotation of Drosophina melanogaster genome.,
"Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                         MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                          SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 NDMNLRWNSSEFGGVRDLRIPPHRLWKPDVLMYNSADEGFDGTYATNVVVRNNGSCLYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGGDISSFVTNGEWELI
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                                 S.E., Gibbs R.A., Rubin G.M., Venter C.J.; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  545;
                                                                                                                        EMBL; AECOBS) to the EMBL/GenBank/DDBJ databases.

R Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

R FlyBase; FR900031014; nACR-alpha-18C.

R FlyBase; CSEGNOSSO: 7 -- CSEGNOSSO: 
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                                                                                                                                                                                                                            receptor activity; IEA
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                                       Adams M.D., Celniker
Submitted (MAR-2000)
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Matches 394; Conserv
                     FROM N.A.
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OSXZI4: 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-UIN-2003 (TrEMBLrel. 24, Last annotation update) Putative nicotinic acetylcholine receptor alpha 7-2 subunit.

Q9XZI4

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                                                                                                                                                                                                                 SEQUENCE FROM N. Adamczewski M.;
SEQUENCE FROM N. Adamczewski M.;
Schulter I., Oellers N., Adamczewski M.;
"Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha? Subunits and C. elegans Ce21 than to char insect nicotinic acetylcholine receptor Alpha subunits.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

C. -- SUBCELBLULAR LOCATION: INTEGRAL MEMBRANB PROTEIN (BY SIMILARITY).

EMBL, AF143847; AAD32698.1; --
RM GO, GO:0016021; C.:Integral to membrane; IEA.

RG, GO:0016221; F:ion channel activity; IEA.

RG, GO:0005216; F:ion channel activity; IEA.

RG, GO:0005216; F:ion transport; IEA.

RG, GO:0005216; P:ion transport; IEA.

RG, GO:0005219; P:extracellular ligand-gated ion channel acti. . .; IEA.

RG, GO:0005216; P:ion transport; IEA.

RG, GO:0005219; P:extracellular ligand-gated ion channel acti. . .; IEA.

RG, GO:0005216; P:ion channel activity; IEA.

RG, GO:0005216; P:ion transport; IEA.

RG, GO:0005217; P:extracellular ligand-gated ion channel activity; IEA.

RG, GO:0005218; P:extracellular ligand-gated ion channel activity; IEA.

REPROFESTION RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 TRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRIDFRRSFVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 APMLAALALILALLPVSEQ-GPHEKRLINALLANYNTLERPVANESEPLEVRFGLTLQQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVDEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPPPDLELRERSSKSLLANVLDIDDDFRH----PQAQQ-----PQCCRY---YRGG---
                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Heliothis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.7%; Score 1803.5; DB 5;
68.7%; Pred. No. 8.9e-167;
ive 53; Mismatches 78;
(Owlet moth)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLIIFTLFTIIATLAVLLSAPHIMV 495
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(Noctuid moth)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGROOB60; LIC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 68.7
Matches 347; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 AA;
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 LQQIIDVDEKNQLLITNLMLSLEWNDYNLRWNETEYGGVKDLRITPNKLWKFDVLMYNSA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21969411; PubMed=11973307; Grauso M., Reenan R.A., Culetco E., Sattelle D.B.; Grauso M., Reenan R.A., Culetco E., Sattelle D.B.; Subveil Putative Nicotinic Accylcholine Receptor Subunit Genes, Dalphas, Dalphas, and Dalphar, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-1 Pre-mRNA Editing."; Genetics 160:1519-1533 (2002).

-: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-: SUBLIARITY: BELCOMICS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SPLPASLSLFVLLIFLAIIKESCQGPHEKRLINHLLSTYNTLERPVANESEPLEVKFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 SHLAAPAGLLLLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 NLIVECVLISSMALLGFTLFPDSGEKLTLGVTILLSLTVFLNLVAESMPTTSDAVPLIGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REMEL, AFF321446, AAMIJ393.1; -...
RIYBASE; FEGUN032151; nAcR-alpha-30D.
ROGO GO:0016621; clintegral to membrane; IEA.
ROGO GO:0016621; clintegral to membrane; IEA.
ROGO GO:0005230; F:extracellular ligand-gated ion channel acti...;
ROGO GO:0005240; F:ion channel activity; IEA.
ROGO GO:0005240; F:ion channel activity; IEA.
ROGO GO:0005694; F:ion transport; IEA.
ROGO GO:0006811; P:ynappric transmitter receptor activity; IEA.
ROGO GO:0006811; P:ynappric transmission; IEA.
ROGO GO:0006811; P:ynappric transmission; IEA.
RITHEPPO: IPR006201; Neur_channel.
RITHEPPO: IPR006202; Neur_channel.
ROGO GO:0000831; Neur_channel.
REMENTY. IPR006202; Neur_channel.
REMENTY. IPR006203; Neur_channel.
                                                                                              01-JUN-2002 (TERBLrel. 21, Last sequence update)
01-JUN-2003 (TERBLrel. 24, Last sequence update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type II.
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG1128.
Drosophila melanogaster (Fruit fly)
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygicia Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 AA; 56048 MW; 6EE711810EDE7BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.4%; Score 1795.5; DB 5;
68.1%; Pred. No. 5.3e-166;
ive 54; Mismatches 81;
                                                           494 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGRO0860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 68.1
Matches 342; Conservative
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane
                                                                          Q8T7S2;
01-JUN-2002
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                                                     Q8T7S2
RESULT 6
281732
10 01-7
20 081732
DT 01-7
DT 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics 160:1519-1533(2002).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; AF321447; AAM13394.1; -.
FINEL; AF321447; AAM13394.1; -.
FINEL; AF321447; AAM13394.1; -.
FO GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:00162216; F:sortracellular ligand-gated ion channel acti. . .; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
GO; GO:0007268; P:synaptic transmission; IEA.
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                                   367 PARVP-PPPDLELRERSSKSLLANVLDIDDDFRHPQAQQPQCCRYYRGGEENGAGLAA--
                                                                                                                   HSCFGVDY-ELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21969411; PubMed=11973307; Grauso M., Reenan R.A., Culetto E., Sattelle D.B.; Grauso M., Reenan R.A., Culetto E., Sattelle D.B.; Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalphas, Dalphas and Dalphaf, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-Coll Pre-mRNA Editing.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 SHLAAPAGLLLLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygol
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidas; Drosophilidae; Drosophila.
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55; Mismatches
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InterPro; IRR006029; Neu channell memb.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan memb; 1.
PRINTS; PR00252; NRĪONCHĀNNEL.
                                                                                                                                                                                                                              474 IFTLFTIIATLAVLLSAPHIMV 495
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472 VFTLFTIIATVTVLLSAPHIIV 493
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InterPro; IPR006202; Neur chan LB
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246

306 302 362 423 473

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MEDLINE-21966411; PubMed=11973307;
MEDLINE-21966411; PubMed=11973307;
Acauso M., Reenan R.A., Culetto E., Sattelle D.B.;
Acauso M., Reenan R.A., Culetto E., Sattelle D.B.;
Acauso M., Reenan R.A., Culetto E., Sattelle D.B.;
Acauso M., Reenan R.A., Culetto E., Subunit Genes,
RT "Movel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphae and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
Mediated A-to-I Pre-mRNA Editing.";
Genetics 160:1519-1533 (2002)
C. -- SUMCELUTAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
C. -- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
C. -- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
C. -- SIMILARITY: PRELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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C. -- SIMILARITY: PRELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
C. -- SIMILARITY: PRODOS216; Fiston channel activity; IBA.
GO; GO:0005216; Fiston channel activity; IBA.
GO; GO:0005216; Fiston channel activity; IBA.
GO; GO:0007268; Piston channel activity; IBA.
MINEPRO; IPROG620; Neur channel.
DR FinterPro; IPROG620; Neur channel.
DR Fian; PPO2931; Neur chan LBD; 1.
R Ffam; PPO2932; Neur chan LBD; 1.
R Ffam; PPO2932; Neur channel.
DR FRAMYS; PRO0225; NEUR-CHANNEL.
DR FRAMYS; TIGRROB60; LIC; 1.
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LMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA
                        DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL
                                                                                                                          DEGFDGTYHTSVVVKHGGSCLYVPPGIFKSTCKMDITWFPFDDQHCEMKFGSWTYDGNQL
                                                                                                                                                                                        DLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFF
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                       247 NLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGT
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Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nicotinic acetylcholine receptor subunit Dalpha6 precursor.
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68.1%; Pred. No. 1.3e-165;
-. v.cmarches 81; Indels
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Signal; Receptor.
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                                                                                                                                                                                                                                                                                                                                                       DEGPDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 YFNCIMEMVASSVVITVVVINYHHRTADIHEMPPMIKSVFLQWLPWILKMGRPGRKITRK 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 TILLSNRMKELELKERSSKSLLANVLDIDDDFRHTIS------GSQTAIGSSASF 411
                                                                                                                                                                                              99
                                                                                                                                                                                                                                  62
                                                                                                                                                                                                               LQQIIDVDEKNQILTTNAWLNLEWNDYNLRWNETEYGGVKOLRITPNKLWKEDVLMYNSA
                                                                                                                                                                                                                                                                                                                                                                               247 NLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVARTMPATSDAVPLLGT
                                                                                                                                                                                     SHLAAPAGLLLLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                                                                                                                         LMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                       DLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNÇCPEPYIDITFAVVIRRKTLYYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 NLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 PARVP-PPPDLELRERSSKSLLANVLDIDDFRHPQAQQPQCCRYYRGGEENGAGLAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------HSCFGVDY-BLSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLI
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEMONING FACURE AND STRUCTURE STRUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type IV.
                                                                                                                                                  25;
                                                                                                            494;
PROSITE; PS00236; NEUROTR ION CHANNEL; 1. Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalphas subunit variant ty
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
                                                                                                            Length
                                                                                                                                                  83; Indels
                                                                B46EBEDA63A92942 CRC64;
                                                                                                       DB 5;
                                                                                                       67.2%; Score 1790.5; DB 5, 67.9%; Pred. No. 1.6e-165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              509 AA.
                                                                                                                                              53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 IFTLFTIIATLAVLLSAPHIMV 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHILLINITY TATES APHILY
                                                              494 AA; 56095 MW;
                                                                                                                         Local Similarity 67.9 es 341; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                           Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                         187
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                                                              SEQUENCE
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                                                                                                         Query Match
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                                                                                                                           Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----HSCFGVDY-ELSLILKEIRVITDQMRKDDEDADISR 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                 IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 SHLAAPAGLILLICLIMPRGARC-GYHEKRLIHHLIDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SPLPASLSLFVLLIFIAIIKESCQGPHEKRLLNHLLSTYNTLERPVANESEPLEVKFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- DEKNOLLITNIWLKLEWNDMNLRWNTSDFGGVKDLRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 LQQIIDVDEKNQILITINAMLNLDEKNQLLITINLMLSLEWNDYNLRWNETEYGGVKDLRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 PHRLWKRDVLMYNSADEGFDSTYPINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 CEMKFGSWTYDGYQLDLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 CEMKFGSWIYDGNQLDLVLNSEDGGDLSDFIINGEWYLLAMPGKKNTIVYACCPEPYVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 TFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                         ·:
·
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .;
R GO; GO:0005216; F:ion channel activity; IEA.
R GO; GO:0005216; F:ion channel activity; IEA.
R GO; GO:0006311; P:ion transport; IEA.
R GO; GO:0007268; P:synaptic transmission; IEA.
R InterPro; IPRO06201; Neur channel.
R InterPro; IPRO06202; Neur channel.
R InterPro; IPRO06202; Neur channel.
R Ffam; PRO2931; Neur chan LBD.
R Ffam; PRO2931; Neur chan LBD; 1.
DR Pfam; PRO2931; Neur chan LBD; 1.
DR Pfam; PRO2932; Neur chan memb; 1.
DR Pfam; PRO2932; NEUCHANNEL.
DR TIGRFAMS; TIGRO0860; LIC; 1.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type NACR-ALPHA-30D OR NACRALPHA-30D OR NACRALPHA-30D OR NECHALPHA-30D OR NECHALPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        509 AA; 57887 MW; BE8D8E0198E0C2BD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.6%; Score 1774; DB 5; 66.0%; Pred. No. 6.9e-164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 523 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Ionic channel; Postsynaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similaricy conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 MPPWIKSVFLQWLPWILKMGRPGRKITRKTILLSNRMKELELKRRSSKSLLANVLDIDDD 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEGFDSTYPINVVVRNNGSCLYVPPGIFKSŢCKIDITWFPFDDQRCEMKFGSWTYDGYQL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEGFDGTYHTNIVVKANGSCLYVPPGIFKSTCKMDITWPPFDDQHCEMKFGSWTYDGNQL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLQLQDEGGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PLLGTYFNCIMFMVASSVVSTILILNYHHRHADTHE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP-PPPDLELRERSSKSLLANVLDIDDD 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELQFIT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMQIIDVDEKNQLLITUIWLKLEWNDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----HSCFGVDY-ELSLILKEIRVIT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHLAAPAGLILLICLIWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLVLNSEDGGDLSDFIINGEWYLLAMPGKKKNTIVYACCPEPYVDITFTIQIRRRTLYYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQQIIDVDEKNQILTTNAMLNLEWNDYNLRWNETEYGGVKDLRITPNKLWKFDVLMYNSA
                                                                                         Dalphas, Dalphae and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-1 Pre-mRNA Editing."; Genetics 160:1519-1533 (2002).
-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
EMBL, AF321449; AAM13396.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLPASLSLFVLIFLAIIKESCQCPHEKRLLNHLLSTYNTLERPVANESEPLEVKFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Gaps
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Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0032151; nAcR-alpha-30D.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:00160230; F:extracellular ligand-gated ion channel acti.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
GO; GO:0006811; F:ion transport; IEA.
GO; GO:0007268; P:synaptic transmission; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.4%; Score 1769; DB 5;
64.4%; Pred. No. 2.2e-163;
tive 53; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_channel.
InterPro; IPR006202; Neur_channel.memb.
Pfam; PP02931; Neur_chan LBD; 1.
Pfam; PF02932; Neur_chan LBD; 1.
PRINTS; PR02022; NEUNCHANNEL.
ITGRFAMS; TICRO0860; LIC; 1.
PROSITE; PS00226; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 FRHPQAQQPQCCRYYRGGEENGAGLAA-
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Best Local Similarity
Matches 342; Conserv
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RX MEDLINE=20196006; PubMed=10731132;

RAMIN=SERVEALEY;

RAMAIN=SERVEALEY;

RAMAIN=SERVEALEY;

RAMAIN=SERVEALEY;

RAMAIN GEORGE P. G. Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F.F.,

GUTCOG, G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D.,

RAMAIN R.C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,

RAMA Ballew R.M., Basus H., Baxendale J., Baraktaroglu L., Beasley E.M.,

RADIU J.F., Mabayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RADIU J.F., Benos P.V., Berman B.P., Bandari D., Boltakavy S.,

Berkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,

RADORON K., Doup L.E., Downes W., Dugan-Rocha S., Punkov B.C., Dunn P.,

RADUDIN K.J., Evangelista C.C., Ferraz C., Gun P., Harris M.,

RADUDIN K.J., Banos P.W., Howland T.J., Hernandez J.R., Houck J.,

RADUDIN K.J., Harvy D., Helman T.J., Hernandez J.R., Houck J.,

RADUDIN K.J., Harvy D., Helman T.J., Hernandez J.R., Houck J.,

RADUDIN K.J., Harvy D., Helman T.J., Hernandez J.R., Houck J.,

RADUDIN K.J., Harvy D., Helman T.J., Horly D., Lai Z.,

Jalai M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,

Liu X., Mattei B., McIntoen T.C., Morist S., Kulp D., Lai Z.,

Liu X., Mattei B., McIntoen T.C., Morist S., Kulp D., Lai Z.,

Liu X., Mattei B., McIntoen T.C., Morist S., Kulp D., Lai Z.,

Radeson D.R., Nelson N.A., Mixon K., Musshern D.R., Pacleb J.M.,

Radeson D.R., Nelson K.A., Mixon K., Musshern D.R., Pacleb J.M.,

Radeson D.R., Nelson N.A., Nixon K., Musshern D.R., Pacleb J.M.,

Radeson D.R., Wassarman D.A., Weinstcok M., Weissenbach J.,

Radeson D.R., Wassarman D.A., Weinstcok M., Wainstenbach J.,

Radilam S.M., Woodage T., Simpson M., Strong R., Wang X., Sunk R.,

Radibas R., Tector C., Turner R., Venter E., Wang X., Zhu X., Smith H.O.,

Radibas R., Jenser S., Shan M., Zhong W., Zhong C., Sheeler F., Shen H.,

Radibas R., Woodage T., Worley K., Sink B., Shue B., Shong S., Shong S., Shen S., Polland S., Shang S., Polland S., Shang S., Polland S., Shang 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

By Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Branson J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Antloon J.W., Center A., Champe M., Davenfort L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Androsh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Milliams Y., Houck J., Park S., Patel S., Frichards S., Scheeler F.,

Racleb J., Paragas V., Park S., Patel S., Richards S., Scheeler F.,

Requencing S., Pittman G.S., Swith H.O., Venter J.C., Rubin G.M.;

T. "Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Héxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CG4128 protein.
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
                                                                   Last sequence update)
Last annotation update)
554 AA.
                                                                                                                                                              Drosophila melanogaster (Fruit fly).
                                           Created)
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                                           13,
                                           (TrEMBLrel.
                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             STRAIN=Berkeley;
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                                           01-MAY-2000
                                                                   01-OCT-2002
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346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLQLQDEGGGDISSFVTNGEWELIGV-PGK-------RNEIYYNCCPEPYIDI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 -----ILFFQFN----CAMCANLIDGPTGLHIAAGFGRETDAGRNYTTIINSISKP 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 CRRVHADNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQCRAERVTILLSLTVFLNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
SEQUENCE FROM N.A.

Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Bane B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                     Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.7%; Score 1484.5; DB 5; Length 554; 53.6%; Pred. No. 1.3e-135; ive 53; Mismatches 98; Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PWILRMGRPGRKITRKTILLSNRMKELELKERSSKSLLANVLDIDDFRHTIS-
                                                                                                                                                                                                                                                                                                    Figure (SEP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003626; AAF52817.2; -...

EMBL; AE003626; AAF52817.2; -...

R 19/Bases; FEBDM032151; hack-alpha-30D.

GO; GO:0016620; C:membrane; IEA.

GO; GO:0016529; F:extracellular ligand-gated ion channel acti

R GO; GO:0016629; F:nourchanemitter receptor activity; IEA.

InterPro; IPR00620; Neur_chanlbD.

R InterPro; IPR00620; Neur_chanlbD.

R InterPro; IPR00620; Neur_chanlbD.

R Pfam; PF02931; Neur_chanlbD: 1.

R Pfam; PF02931; Neur_chanlmemb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0252; NRIONGHANNEL.
TIGREAMS; TIGR00860; LIC; 1.
PROSITE; PSO0236; NEUROTR ION CHANNEL; 1.
SEQUENCE 554 AA; 63236 MW; D6C63EB7F5B32A35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 53.68
Matches 310; Conservative
                                                                                                                                                                                                                                                        [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                  SEQUENCE FROM N.A.
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RAY SEQUENCE: FROM N.A.

Addams M.D., Celnikers S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Admanstides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanstides P.G., Scherer S.E., Holt R.A., Sahburner M., Henderson S.N.,

RA Danistides P.G., Scherer S.E., In PW, Hoskins R.A., Galle R.F.,

RA Cherton G.G., Wortman J.R., Plazel R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Daril J.F., Agbayani A., Am H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Bancs P.V., Barter E.G., Helf G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., Am H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Bancs P.V., Bernal B.P., Bhandari D., Boltakov S.,

RA Beson K.Y. Benos P.V., Bernal B.P., Bhandari D., Boltakov S.,

RA Borkova D., Botcher A., Bouck J., Brokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Glodek A., Gody F., Gorner H., Gargen R.S., Fleischmann W.,

RA Glodek A., Gody F., Gorner J., Hornandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wal M.H., Ibeyama C.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechnison J.A.,

RA Harris N.L., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Harris N.L., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,

RA Bazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resenber M.S.,

Rabson D.R., Malson R.A., Nixon K., Nixon M., Strong R., Sun E.,

Spier E., Spradin-Klamos I., Simpson M., Strong R., Sun E.,

Spier E., Spradin-Klamos I., Simpson M., Strong R., Sun E.,

Spier E., Spradin-Klamos I., Simpson M., Strong R., Sun E.,

Spier E., Shodister C., Wund S., Zhu K., Shilth H.O.,

RA Shue B.C., Siden-Klamos I., Simpson W., Sungski M., Sinkh H.,

RA Shen S.M., Woodager, Worley K.C., Wu D., Yang S., Yoo Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128
                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
458 RDWKFAAMVVDRLCLIIFTLFTIIATLAVLLSAPHIMV
                                           516 GDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIV
                                                                                                                                                                                                                                                              PRELIMINARY;
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Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Baracon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Liegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Wurphy B., Nelson C., Nelson K.A., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

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310 ATVWVLQYHYHDPEGGKMPKWTRVVLLNWCAWFLRMKRPGEDKVRPACHNKQPRSSLSSV 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              509 AA; 58056 MW; 1BF152F4245578BA CRC64;
400 RMKELELKERSSKSLLANVLDIDDDFRHTIS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                                                     Created)
                                                                                     IIATLAVLLSAPHIMV 495
                                                                                                    01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                     Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261
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Best Local S
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 DEGEDGTYHTNIVVKHNGSCLYVPPGIFKSTCKIDITWFPFDDOHCEMKFGSWTYDGNQL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TILLSLTVFLNMVAETMP-----ATSDAVPLLGTYFNCIM 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLQLQDEGGGDISSFVTNGEWELIGV-PGK------RNEIYYNCCPEPYIDI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FMVASSVVSTILLILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARVP- 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                .; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHLAAPAGLILLLCLLWPRGARC-GYHEKRLLHHLLDHYNVLERPVVNESDPLQLSFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ILFFQFN----CAMCANLIDGPTGLHIAAGFGRETDAGRNYTTIINSISKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                    SEQUENCE FROM N.A.
Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Tradecky P., Huany Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield B., Ashburner M., Gelbart W.M., Rubin G.M., Munogall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 TFAVVIRRKTLYYFFNLIVPCVLIASM-----ALLGFTLPPDSGEKLSLGV---
Phouanenavong S., Pittman G.S., Furi V., Richards S., Scheeler F. Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 525;
                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. MEML; ABOD3626; ABN10709.1; -..
FlyBases; FBGN0032151; nAcR-alpha-30D.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005220; F:extracellular ligand-gated ion channel a GO; GO:0005230; F:neurotransmitter receptor activity; IEA.
GO; GO:0006811; P:ion_transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRRVHADNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQCRAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF95283C56EA90A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.4%; Score 1371; DB 5;
52.2%; Pred. No. 1.4e-124;
tive 56; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006201; Neur_channel.
InterPro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_channel.
FinterPro; IPR006029; Neur_chan_IBD.
Ffam; PF02931; Neur_chan_IBD; 1.
PRINTS; PR00252; Neur_chan_memb; 1.
PRNOSITE; PS00253; NEUNOTR. ION CHANNEL; 1.
SEQUENCE 525 AA; 60135 WW; CF95283C56EA
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-GSQTAIGSSASFGRPTTV 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132
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                                                           ---HSCFGVDY-ELSLILKEIRVITDQMRKDDEDADISRDWKFAAMVVDRLCLIFTLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLLWPRGARCGYHEKRLLHHILDHYNVLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLL
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190 YIANGEWDLVEVPGRRNERFYDCCKEPYPDVTFTVVMRRRTLYYGLNLLIPCVLISTLAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Zirger J.M., Boyd R.T.; Zirger J.M., Boyd R.T.; "Cloning and expression of zebrafish neuronal nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0TM-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Nicotinic acetylcholine receptor alpha 7 subunit.
Brachydanio rerio (Zebrafish) (Banio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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BMBL; AY247962; AA03913.1; -.

BMBL; AY247962; AA03913.1; -.

GO; GO:0016220; C:membrane; IEA.

GO; GO:0016230; F:extracellular ligand-gated ion channel acti...;

RO; GO:0005230; F:extracellular ligand-gated ion channel acti...;

RO; GO:0005230; F:extracellular ligand-gated ion channel acti...;

RO; GO:0006811; P:ion transport; IEA.

RIPEPPO; IPR006201; Neur channel.

RIPEPPO; IPR00622; Neur channel.

RP Fam; PF02393; Neur chan LBD; 1.

RP Fam; PF02392; Neur chan LBD; 1.

RP RINTS; PR00252; NRIOWHANNEL.

R TIGREPMS; TIGRO860; LIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 509;
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al Similarity 50.0%; Pred. No. 5.2e-115;
247; Conservative 87; Mismatches 133; Indels
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DLNISPGVAQSTNGNLLYI--GFRGMDTIH-YATSPDSGVICSRLVATGEEDVLLPGAQA 426
                                                                                                                                    SSVSSSGPGETELSKILDEVRYISKRFRDQDEEDTVCNEWKFAASVIDRLCLMAFSLFII 486
          ---GAGL 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NDMNLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGIFKSTCKIDITWPPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGGDISSFVTNGEWELL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIASMALLGFTLPPDSG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKLSLGVTIILSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHH 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HDPNGGNMPKMVQLVLLQWVAWFLRMKRPGEKDSPERPPCAPHLRRCSSGSSGSIPNPP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---RERSSKSLLANVL-----DIDDDFRHPQAQQ-- 404
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                                                                                                 AAHSCFGV-DYELSLILKEIRVIIDQMRKDDEDADISRDWKFAAMVVDRLCLIIFTLFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
DLELRERSSKSLLANVLDIDDFR-----HPQAQQPQ----CCRYYRGGEEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.0%; Score 1253; DB 13; Length 555;
44.7%; Pred. No. 4.7e-113;
ive 86; Mismatches 126; Indels 92
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Nicotinic acetylcholine receptor alpha 7b subunit (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
555 AA; 61010 MW; B042A3E4430A2B7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                555 AA.
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LCTIGILMSAPNFV 500
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EMBL; AY298752; AAP57216.1;
                                                                                                                                                                                                        481 IATLAVLLSAPHIM 494
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SEQUENCE
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GenCore version 5.1.6
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protein - nucleic search, using frame_plus_p2n model

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8, 2004, 11:50:34 May Run on:

; Search time 3463.3 Seconds
(without alignments)
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27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

em_estba:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		19 GH16126	D013901 901345	02873 Homo sa	53497 Mus mu	51730 Mus mu	0415 Mus mus	299 AI,530299	102 Mile 2729	742 Mile	2875 Mis	2878 Mus	9	BU915857 AGENCOURT	0	12 Mus m	7 Mus	475 Mus	877	228 Mus	57 Mus	9013	Mus		Mus	Pan	9013	902 9013	CD013903 90134855	1 9013	4 Mus	T WUS	0 5	25 PATRICULT	U	188 9013880	460 K-EST020	1327 Homo sa	L344 Mus musc	5337 UI-M-FY	3211 Droso	7974 Mus	3676	7186 Mils	2011 0011 001100
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ALIGNMENTS

RESULT 1 BG632919/c

LOCUS

BG632919

GH16126.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster c CG4128: FBan0004128 ion channel located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence. BG632919.1 GI:13758409 ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION

Drosophila melanogaster (fruit fly) Drosophila melanogaster Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

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/mol type="mmrance or process" | /mol type or private or purive Cloning Vector; RT-PCR was performed using gene-specific primers flanking the open-reading frame. PCR products were subcloned into purive Cloning Vector and sequenced completely using M13 forward and reverse primers. Sequencing gaps were closed by re-sequencing using primers flanking the gapped areas."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.

1 (bases 1 to 2296)
1 (bases 1 to 2296)
2 (bip.P., FwiG.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R., Au-Young,J. and Stuve,L.L.
PCR isolation and cloning of novel splice variant mRNAs from known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 IleLeuAsnTyrHisHisArgHisAlaAspThrHisGluMetSerAspTrpIleArgCys 344
                                                                                                                       145 TITITCAATCTGAITGTGCCGTGCGTACTGATCGCCTCCATGGCACTGCTAGGGITTACA 286
                                                                                                                                                                                                                                                                                      284
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GTCCTCAATTATCATAGAAATCCAGATACGCATGAAATGAGTGAATGGGTA-----
                             PhePheAsnLeuIleValProCysValLeuIleAlaSerMetAlaLeuLeuGlyPheThr
       205 GlyGluTrpGluLeuIleGlyValProGlyLysArgAsnGluIleTyrTyrAsnCysCys
                                                                                                 ProGluProTyrIleAspIleThrPheAlaValIleArgArgLysThrLeuTyrTyr
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CD013301
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3160 Porter Drive, Palo Alto, CA 94304, USA
TE1: 650 621 8639
Fax: 650 621 8965
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Location/Qualifiers
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Unpublished (2003)
Contact: Jin, P.
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/organism="Drosophila melanogaster"
/mol type="mRNA"
/db_xref="taxon:727"
/clone="GH16126"
/sex="male and female"
/dev stage="adult"
/lab host="DH5" - alpha"
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/c
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Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 885)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Euris,S. and Rubin,G.M.
BOGP/HHMI Drosophila EST Project
Unpublished (2001)
Conter_ESTS: GH16126.5prime
Contar_to Stapleton, M.
BDGP
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gene <1>1436 /gene="CHRNA3" /locus_tag="HCM1369"	Alignment Scores: 2.75e-76 Length: 1436 Score: 942.50 Matches: 194 Percent Similarity: 58.25\$ Conservative: 92 Best Local Similarity: 35.37\$ Indels: 53 DB: 29 Gaps: 6	US-09-303-232-4 (1-496) x AY402873 (1-1436) QY	48 LeuGluargProValValAsnGluSerAspProLeuGlnLeuSerPheGlyLeuThrLeu :::	Qy 68 MetGlnIleIleAspValAspGluLysAsnGlnLeuLeuIleThrAsnIleTrpLeuLys 87 Db 123 TCTAGCTGGTGAAGGAGAACAAACCAGATGAAGACCAACCTGGACCAACCTGGAGCTGAAG 182 Qy 88 LeuGluTrpAsnAspMetAsnILeuAspTrpAsnThrSerAsppheGlyGlyValLysAsp 107 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 183 CAAATCTGGAATGACTACAAGCTGAAGTGGAACCCCTCTGACTATGGTGGGGCAGAGTTC 242 Qy 108 LeuArgValProProHisArgLeuTrpLysProAspValLeuMetTyrAsnSerAlaAsp 127 Db 243 Angedengengaanananananananananananananananana	128 GluGlyPheAspSerThrTyrProThrAsnValValValArgAsnAsnGlySerCysLeu 100 GluGlyPheAspSerThrTyrProThrAsnValValValArgAsnAsnGlySerCysLeu 100 Global Grandes G	148 TyrvalProProGly1lePheLysSerThrCysLys1leAsplleThrTrpPheProPhe 1363 TGGATACCTCGGGCATTTTAGAGACTCCTGTAAAAATCGACGTGACCTACTTCGTTTAAAAACGGTCATTCCGGTTA	168 AspaspGlnArgCysGluMetLysPheGlySerTrpThrTyrAspGlyTyrGlnLeuasp 	Oy 188 LeuGlnLeuGlnAspGluGlyGlyGlyAspIleSerSerPheValThrAsnGlyGluTrp 207	Qy 208 GluLeuileGlyValProGlyLysArgAsnGluileTyrTyrAsnCysCysProGluPro 227 Db 540 GCCATCATCAAAGCCCCAGGCTACAAACACGACAACAAGAAGTACAACTGCTGCGAGGAGATC 599		Oy 248 LeuileValProCysValLeuileAlaSerMetAlaLeuLeuGlyPheThrLeuProPro 267	Oy 268 AspSerGlyGluLysLeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeu 287	Qy 288 AsnMetValAlaGluThrMetProAlaThrSerAspAlaValProLeuLeuGlyThrTyr 307 :::::	308 PheAsnCyslleMetPheMetValAlaSerSerValValSerThrIleLeulleLeuAsn 32

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MRVPAEKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKITOVTYF
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Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Oneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatun, N., Hiramoto, K., Hiracka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kothihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Shibatta, K., Shinagawa, A., Shiraki, T., Takeda, Y., Tanaka, T., Tagawa, A., Takahashi, F., Takahira, S., Murata, M., Makani, M., Tagawa, A., Takahashi, F., Takahira, S., Miramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
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Analysis of the mouse transcriptome based on functional annotation Nature 420, 563-573 (2002)

( (bases 1 to 1864)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Please visit our web site for further details.
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/db_xref="MGI:24<u>5</u>5288"
/db_xref="taxon:10090"
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URL:http://fantom.gsc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||| | :::::::||||||| 475 GATGACAAAAACCAAAGGCTTTGGATCCCTCCGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 GluMetLysPheGlySerTrpThrTyrAspGlyTyrGlnLeuAspLeuGlnLeuGlnAsp
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/note="putative"
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                                                                                                      polyA_signal
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Nature 420, 563-573 (2002)

E (bases 1 to 2916)

R dacch,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiracka,T., Hirocane,T., Karukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Konda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Mixata,M., Nakamira,M., Nishi,K., Nomuraki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakaume,N., Saraki,D., Shibata,K., Shinagawa,A., Shiraki,T., Takeda,Y., Tanaka,T., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takada,Y., Tanaka,T., Tomaru,A., Takahashi,F., Takaku-Akahira,S., Miraki,M., A., Takahashi,F., Takaku-Akahira,S., Miraki,M., A., Toya,T., Yasunishi,A.,
                                                                  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watchiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIXEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIXEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseges.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Enomials Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                   The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 .1669
/note='unnamed protein product; NEURONAL NICOTINIC
ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AAL58471,
evidence: FASTY, 99.8%ID, 100%length, match=1497)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Please visit our web site for further details.
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/strain="C57BL/6J"
/db_xref="FRATOM DB:D130068A06"
/db_xref="mRG1:242066"
/db_xref="taxon:10090"
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/clone_lib="RIKEN full-length
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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Mus musculus 12 days embryo spinal ganglion cDNA, RIKBM Full-length enriched library, clone:0130068AG6 product:REURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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                                                                                                                                                   353 ValleuArgMetSerArgProGlySerAlaThrThrProProProAlaArgValProPro 372
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
LeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGlu 292
                                  1012 ATTTTTGTCACCTTGTCCATCGTCATCACGTCTTTGTGCTCAACGTGCACTACAGAACT
                                                                                                                                                                                                                                                                                                                                       333 AlaAspThrHisGluMetSerAspTrpIleArgCysValPheLeuTyrTrpLeuProTrp
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                                                                                                                ThrMetProAlaThrSerAspAlaValProLeuLeuGlyThrTyrPheAsnCysIleMet
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AK051730.1 GI:26
HTC; CAP trapper.
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ATTTTTGTCACCTTGTCCATCGTCATCACAGTCTTTGTGCTCAACGTGCACTACAGAACT 1147
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GTCATGTTTATGACTAGGCCA-----ACCAGCACCGAGGAAGACGCCCCCAAAG 1255
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                                                                                                                                                                                                                                                                            AlaAspThrHisGluMetSerAspTrpIleArgCysValPheLeuTyrTrpLeuProTrp 352
                                                                                                                                                                                                                                                                                                                                         ValLeuArgMetSerArgProGlySerAlaThrThrProProAlaArgValProPro 372
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Sciurognathi, Muridae, Murinae, Mus.
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   TACTCGCTATACATTCGCCGCCTGCTGTTCTACACCATCAACCTCATCATTCCGTGC
                               ValLeulleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLys
                                                                                          LeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGlu
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3126 bp mRNA linear HTC 19-SEP-Misseculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730007P14 product:NBURONAL NCOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
                                                                                                                                                       ThrMetProAlaThrSerAspAlaValProLeuLeuGlyThrTyrPheAsnCysIleMet
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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| ATTTTAGGAACTGCAGGATTATTTCTG 1639
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Rodentia;
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AK080415.1 GI:26348538
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata
Mammalia; Eutheria; Rodentia
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                                     /protein_id="BAC34740.1"
/db_xref="G1:26342156"
/translation="MGVVLPPPPLSMLMLVLMLLPVASASEAEHRLFQYLFEDYNEII
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L. Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genome Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@ges.riken.go.jp, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                       Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-184-format Genome Res. 10 (11), 1757-1771 (2000)
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/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="7 days neonate"
                                                                                           genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation 6 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3126)
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            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
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Please vieit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/db_xref="MGI:2407635"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                           YNEI IRPVANVSHPVI IQFEVSMSQLVKVDEVNQIMETNLWLKQIWNDYKLKWKPSDY
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                                                                                                                                                                                                                                                                                                                                               DVTY FPFDYQNCTMKFGSWSYDKAKIDLVIJGSSMNLKDYWESGEWAJIKAPGYKHEI
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/note="unnamed protein product; NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AAL58471, evidence: FASTY, 99.8%ID, 100%length, match=1497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 GTGGATGAAGTAAACCAGATCATGGAAACCTGTGGCTGAAGCAAATCTGGAATGAC
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/tissue type="NEUROBLASTOMA COT 50-NORMALIZED" /clone lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED" /note="Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and cloned into the Not I and strand sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                     was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7646.r For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
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                                                                                                                                                                                                                              http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODD007CH03QPl&cluster=7646.r. Contac
cgi-bin/cluster.cgi?seq=CSODD007CH03QPl&cluster=7646.r. Contac
Feng Liang Email : fliangalifecch.com/URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODD007CH03QPl.
Location/Qualifiers
                                                                                 Contact: Genoscope
Genescope - Centre National de Sequencage
BP 19 91006 EYRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                                                                    gi:12793792
                                                                On Feb 13, 2001 this sequence version replaced
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175
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  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Mismatches:
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                                            844
                                                                                                                                                                                           313 PheMetValAlaSerSerValValSerThrIleLeuIleLeuAsnTyrHisHisArgHis 332
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
                                                                               PheAlaValValIleArgArgLysThrLeuTyrTyrPheAsnLeuIleValProCys
                                                                                                         ProGlyLysArgAsnGluIleTyrTyrAsnCysCysProGluProTyrIleAspIleThr
                                       ccedectracaracardaarcargracaactrecterereagadarctaccaagacarcace
                                                                                                                                                                   ValleulleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLys
                                                                                                                                                                                                                                                       LeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGlu
                                                                                                                                                                                                                                                                                                                                        ThrMetProAlaThrSerAspAlaValProLeuLeuGlyThrTyrPheAsnCysIleMet
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ATTTTAGGAACTGCAGGATTATTTCTG 1636
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Group Phase I E II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

E (bases 1 to 4037)

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E (bases 1 to 4037)

E (bases 2 to 4037)

E (bases 3 to 4037)

E (bases 3 to 4037)

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Adachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W.,

Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,

Hayashida,K., Hayatsu,N., Hiramcto,K., Hiracka,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,

Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,

Nakamura,M., Nishi,K., Nomura,Y., Kondo,M., Ohsato,N.,

Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,

Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,

Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,

Muramatsu,M. and Hayashizaki,Y.
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//protein id="BA033893.1"
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/db xref="01:26340460"
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LINEARINGSELVTYOLMVSIAQLISYHEREOIMTYWWITOEMEDYRLTWKEEDEDIM
KKVRLPSKHIMLPDVVLYNNADGMYEVSFYSNAVVSYDGSIFWLPPAIYKSACKIEVK
HEPFROQNCTWKRENAYYDRTEIDLVLKSDVASLDDFTSGSWD11ALDGRANBNPDD
STYVDITYDFIIRREPLFYTINLIIPCVLITSLAILVFYLESBCGERGYTLCISVLAL
TVFLLLISYUPTLEFCHOURHKCARQHIKLRFRQFEREGGGTLLFFREGFRADFOTTCFVN
VKVVFDEKLPFTLLFLQDFHRCARQHIKLRFRQFEREGGGTLFFREGFRADFOTTCFVN
PASMGGLAGAFQAEBAAGLGRSMGECSCGLREAVDGVRFIADHMRSEDDDGSVREDM
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (16-UUL-2001) Yoshinide Hayashizaki, The Institute of Submitted (16-UUL-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URi:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                      The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                 Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KYVAMVIDRLFLWIFVFVCVFGTIGMFLQPLFQNYTATTFLHSDHSAPSSK"
                                                                                                                                                     Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                 Group Phase II
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/db_xref="MGI:2417229"
/db_xref="taxon:10090"
                                                                                                 The RIKEN Genome Exploration Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/strain="C57BL/6J"
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                                                                                                                              FANTOM Consortium.
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Mus musculus 12 days embryo spinal cord coln4, RIKEN full-langth enriched library, clone:C530044F16 product:Cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
763 AAAGAGCCCTACCCCGATGTCACCTTCACAGTGACCATGCGCGCAGGACGCTCTACTAT
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                                                                                              GlnLeuAspLeuGlnLeuGlnAspGluGlyGlyGlyAspIleSerSerPheValThrAsn
                                                                                                                                                                                                                         GlyGluTrpGluLeulleGlyValProGlyLysArgAsnGluIleTyrTyrAsnCysCys
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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1062 TCGTGCTGCAGTACCAC 1078
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, Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
1 subtraction of cap-trapper-selected cDNAs to
1 th cDNA libraries for rapid discovery of new genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Indocatory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 4046)
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nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891,
GB|NM_009602, evidence: BLASTN, 99%, match=1498)
                                                                                                                                                                                                    The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
--yuencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861
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Please visit our web site for further details.
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URL:http://fantom.gsc.riken.go.jp/
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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 CTCGACGTACCGCTGGTGGGAAAGTACCTCATGTTCACCATGGTGGTGCTAGTCACCTTCTCC
                                                            SerAspTrpIleArgCysValPheLeuTyrTrpLeuProTrpValLeuArgMetSerArg
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Mus musculus CHRNA3 gene, VIRTUAL TRANSCRIPT, partial sequence
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Mismatches:
Indels:
Gaps:
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314 MetValAlaSerSerValValSerThrIleLeulIeLeuAsnTyrHisHisArgHisAla 333	ProAspLeuGluLeuArgGluArgSerSerLysSerLeuLeuAlaAsnValLeuAspIle 393 ::: AGGAACTTCTACGGTGCTGAGCTCTAAACTGAACTGCTTCAGCCGTGCAGACTCCAAA 108 AspAspAspPheArgHisProGlnAlaGlnGlnProGlnCysCysArgTyrTyr 411	AGCTGCAAGGAAGGCTACCC- ArgGlyGlyGluGluAenG AGGGTAAAAATCTCAAATTTCA	430 AsptyrGluLeuSerLeu	461 LysPheAlaAlaMetValValAspArgLeuCysLeuIleIlePheThrLeuPheThrIle 480	AY402878 AY402878 Mus musculus genomic surv	ACCESSION AY402878 VERSION AY402878.1 GI:39758861 KEYWORDS GS. SOURCE Mus musculus (house mouse) ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	⊃ H - 10 O		CORNIAL BURNILLEW (10-YWV-2004) CELETA GENOMICS, 45 WEST GUAGE DIIVE, ROCKVILLE, MD 20850, USA COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers source 11454

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arcatgaccaccaccatctgctaaaacaggaatggact 203
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AAGATAGAGGTGAAGCACTTTCCCTTCGACCAGCAGAAC 443
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                                                                                                                                                                                                                                                                                                         LeuGlnLeuSerPheGlyLeuThrLeuMetGlnIleile
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Mismatches:
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Gaps:
musculus"
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n:10090"
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/clone lib=NUCHD XGC OOI"
/note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1;
/note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1;
cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.2 kb. Constructed by Life Technologies."
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AAGATCGTGCCACCCCCCCTCCCTCGATGTGCCTCTCATCGGCAAGTACCTCATGTTCACC 851
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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1 (bases 1 to 922)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyLeuAlaAlaHisSerCysPheGlyValAspTyrGluLeuSerLeuIleLeuLysGlu
                                MetPheMetValAlaSerSerValValSerThrIleLeuIleLeuAsnTyrHisHisArg
                                                      HisAlaAspThrHisGluMetSerAspTrpIleArgCysValPheLeuTyrTrpLeuPro
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Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LINL at:
http://mage.llh.gov
Plate: LiAM14228 row: f column: 14
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                                                                                                                                                                            TrpValLeuArgMetSerArgProGlySerAlaThrThrPro
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Location/Qualifiers
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BU915857.1 GI:24097771
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                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1374)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferritera, S., Wargo, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. P. Adams, M.D. and Cargill, M. P. Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                                                                                                                                                                                                                                                                                                                                Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                          AY406230 1374 bp DNA linear GSS 15-DEC-
Homo sapiens CHRNAl gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
                                                                                                                                                                                                                                                                        Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Conservative:
Mismatches:
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Science 302 (5652), 1960-1963 (2003)
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/db_xref="taxon:9606"
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/locus_tag="HCM2488"
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TGGCGCCCAGACCTTGTTCTCTATAACAATGCAGATGGTGACTTTGCTATTGTCAAGTTC 375
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              TTCTCCTTCTTAACCAGCCTGGTGTTCTACCTGCCCACAGAGCTCAGGGGAGAAGATGACG
                                                               ThrAsnValValValArgAsnAsnGlySerCysLeuTyrValProProGlyIlePheLys
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                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1374)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, B., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA. This sequence was made by sequencing genomic exons and ordering them based on alignment.
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                                                             AY406232 15-DEC.
Mus musculus CHRNA1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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                                                                                                                                                                                                                                                                                                                                                            Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, W. A., Tanenbaum, D. M., Civello, D. R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
CCTCGGAGTCTTCATGCTTTGCATCATCGGAACCCTAGCCGTG 1335
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Conservative:
Mismatches:
Indels:
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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AY406232.1 GI:39762206
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-303-232-5_COPY_95_1597 1503 1 atggcccctatgttggcggc......caccgcatatcatcgtgcaa 1503 6940544 3470272 seqs, 21671516995 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Title: Perfect score: Scoring table: Sequence: Searched:

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1	
AF143847	
LOCUS	AF143847 3029 bp mRNA linear INV 27-MAY-1999
DEFINITION	Heliothis virescens putative nicotinic acetylcholine receptor alpha
	7-2 subunit mRNA, complete cds.
ACCESSION	AF143847
VERSION	AF143847.1 GI:4895006
KEYWORDS	
SOURCE	Heliothis virescens (tobacco budworm)
ORGANISM	Heliothis virescens
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
	Neoptera, Endopterygota, Lepidoptera; Glossata, Ditrysia;
	Noctuoidea, Noctuidae, Heliothinae, Heliothis.
REFERENCE	1 (bases 1 to 3029)
AUTHORS	Schulte, T., Oellers, N. and Adamczewski, M.

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                               GATGAGGCAGGCGATCTATCGGACTTCATAACAAATGGGGAGTGGTATCTAATAGGA
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Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha
                                                                                                                                                                                                                                                                                                 /protein id="AAD32698.1"
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//db_xref="G1:4895007"
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CDMKFGSWTYDGNQLDLVLKDEAGGDLSDFITNGEWYLLGMPGKKNTITYACCPEPTV
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NLVMETLPQVSDAIPLIGTYRNCIMPWVASSVVLTVVVLNYHRRADIHEMPQMIKSV
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PPNSTASTGWLGPGGSIFRTDFRRSFVRPSTWEDVGGGLGSHRELLLILRELQFTTA
RMKKADEEAELISDWKFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHIIVQ*
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Schulte,T., Oellers,N. and Adamczewski,M.
Direct Submission
Submitted (19-APR-1999) ZF-BTB, Bayer AG,
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Similarity 100.0%; Pred. No. 0;
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                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctucidae; Noctucidae; Heliothinae; Heliothis.

1 (Dases 1 to 3109)

2 Martin,A., Nadja,E. and Thomas S.

Nucleic acid encoding insect actyl choline receptor subunit Patent: JP 2000023680-A 3 25-JAN-2000;

BAYER AG

OS Heliothis virescens
PD 25-JAN-2000
PF 26-APR-1999 JP 1999118159
PR 04-MAY-1998 DE 19819829.9
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/organism="Heliothis virescens"
/mol_type="genomic DNA"
/db_xref="texon:7102"
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E58348.1 GI:13019347
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Heliothis virescens (tobacco budworm)
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DVTFITINIRRPLYYFPNLIVPCVLISSMALIGFTLPPDSGEKLTLGYTILLSCLTVFL
NLVAETLPQVSDAIPLYFNCIMWYSSVVLIVVVLNYHHRTADIHEMPQWIKSV
FLQWLPWILRWSRFDFKLTRKTIMMYRMRELELKRESSKSLLANVLDIDDDFRHGPP
PPNSTASTGNLGPGCSIFRTDPRRSFVRPSTMEDVGGGLGSHRREHLILRELQFITA
RMKKADFERAELISDWKFAAMVVDRFCLFVFTLFTIJATVAVLLSAPHIIVQ"
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                                                                                                               Adamczewski, M.D., Schulte, T.D. and Oellers, N.D.
Nucleic acids encoding acetylcholin-receptor subunits from insects
Patent: EP 0962528-A 5 08-DEC-1999;
BAYER AG (DE)
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Heliothis virescens
Heliothis virescens
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Lepidoptera; Glossata; Dirrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
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ive 0; Mismatches
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/protein_id="CAC07501.1"
/db_xref="G1:9996847"
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/db_xref="d1:20152849"."

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/translation="mansph_basisherUliFlaiIXESCOGPHEKELLNHLLSTYNTL

ERPWANESEPLEVKFGLTLQOIIDVDEKNQLLITNLMLSLEMNDYNLRWNETEYGGVK

DIRITPNKLWKPDVLMYNSADBGFGFGTTHJNLYVBGSGFCTVYPPGFIRSTCKNDITW
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CCPEPYVDITFTIQIRRRILYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
LSLTVFLNLYARTLEQVSDAIPLGTYTYDCINFWASSWYLTVVVLXYHHRTADIHEM
PPWIKSVFLOMLWHINGRPGRKITKTILLSNRWKELELKERSSKSLLANVLDIDD
DFRHTISGSQTAIGSSAASFGRPTYVBEHHTATGCNHKDLHLILKELQFITARNRKADD
EAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ"
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilade; Drosophila,
1 (bases 1 to 2023)
Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
Genetics 160 (4), 1519-1533 (2002)
    nicotinic acetylcholine receptor Dalpha6 [ (nAckalpha-30D) mRNA, complete cds,
                                                                                                                                                                                                                                                                             2 (bases 1 to 2023)
Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
3QX, UK
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compared to the sequence deposited in GenBank Accession
Number AE003626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serine substitution; com
GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3b
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Pred. No. 1.1e-193;
0; Mismatches 393; Indels
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i
                                                                                     Drosophila melanogaster (fruit fly)
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to the sequence deposited
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/mol_type="mRNA"
/db_xref="taxon:7227"
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|qene="nAcRalpha-30D"
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Drosophila melanogasters subunit variant type I: alternatively spliced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 AGAAGAATCAACTACTTATAACCAATATATGGCTGTCGTTGGAGTGGAATGACTACAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAGGTGGAACGACAGCGAGTATGGCGGGGTCAAGGACCTCAGGATCACGCCCAACAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                710 TGTGGAAGCCCGACGTGTCATGTACAACAGCGCGGATGAGGGATTCGATGCCACGTATC
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/protein_id="AaM13392.1"

/db_xxef="df:20152845"
/translation="MDSPLPASLSLPVLLIFLAIIKESCQGPHEKBLLNHLLSTYNTL
ERPWARSEELOWFGHTLQQTIDVDEKNQIITTNAMLNLEWNDYNLRWNETEYGGVK
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PPFDDQHCEMKREDWLAWNSADEGFOGTYTHIVVKHNGSCLYVPPGEIFKSTCKIDITW
CCPEPYVDITFTIJGRRTLYYFENLIVPCVLISSMALLGFTLEPDSGEKLTLGVTI
LSLTYRLNLYARTLEQVSDA.PLLGTYFFNCINFWNASSVYLTVVVLINYHHRTADIHEM
PPHIKSVPLQMLPWILMRRECRYTTRKTILLSNRWASSVYLTVVVLHYHHRTADIHEM
PPHIKSGSQTALGSSASFGRPTTVEEHHTAIGCNHOOLHILLKELGFTTARNKRADD
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                                                                                                                                                                                                                                                                                                                                                        /gene="nAcRalpha-30D"
/note="results in isoleucine to methionine substitution;
compared to variant clone"
/replace="g"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      compared to variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 IGIGGAAGCCGGACGTCCTTAIGTATAATAGTGCTGACGAGGGTTTTGACGGGACCTACC
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                                                                                                                                                                                                                                                          /gene="nAcRalpha-30D"
/note="results in asparagine to glycine substitution;
compared to variant clone"
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/note="compared to variant clone"
/replace="a"
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Pred. No. 1.5e-188;
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/note="compared to variant
/replace="t"
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/gene="nAcRalpha-30D"
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Best Local Similarity 70.1
Matches 1046; Conservative
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/product="nicotinic acetylcholine receptor Dalpha6 subunit
variant type I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster

Busaryota; Metazoas, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophila; Drosophila;
I (bases 1 to 2023)
Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Novel Putative Micotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARNA linear INV 29-APR-2(
Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6
subunit variant type I (nAcRalpha-30D) mRNA, complete cds,
alternatively spliced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 2023)
Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
          1490 AGGAGCTGGAGCTAAAGGAGCGCTCCTCCAAATCCCTGGCCAATGTCCTCGACATCG
                                                    1151 ATGATGACTTCAGACACGGCCCTCCGCCTCCTAACAGTACTGCCTCGACCGGGAATTTGG
                                                                                                                                                                             regaggaggarcacacegccarcegcrecaarcacaagarcricarcraarrinaarc
                                                                                                                                                                                                                                                                                                        AGCTGCAGTTCACGGCCAGGATGAAGAAGGCTGATGAGGAAGCCGAGCTGATCAGCG
                                                                                                                                                                                                                                                                                                                                                    1688 AATTGCAATTTATTACGGCGCGCGATGCGCAAAGCTGACGAAGCGGAATTGATCGGCG
                                                                                                                                                                                                                                                                                                                                                                                         ACTGGAAGTTTGCTGCGATGGTTGTTGATAGGTTTTTGCCTGTTCGTGTTCACACTTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                 1748 ATTGGAAGTTCGCGGCAATGGTTGTGGATAGATTTTTGTTTAATTGTTTTCACGCTCTTCA
                                                                                                                                   TGGAAGACGTGGGCGGCCTGGGTAGCCACCATCGCGAGCTGCACCTCATACTGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATTATTGCAACGCTTACGGTGCTCTCCCGCTCCGCACATAATCGTGCAA 1860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
mol_type="mRNA"
db_xref="taxon:7227"
/chromosome="2"
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	AF321446 AF321446 ION Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type II (nAcRalpha-30D) mRNA, complete cds, alternatively spliced. ON AF321446.1 GI:20152846	-	Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B. Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing Genetics 160 (4), 1519-1533 (2002)		Genetics U 3QX, UK I rce	/ Organism="Drosophila melanogaster" /mol_type="mnNA" melanogaster" /db_xref="taxon:7227" /chronisome="2"	/ map= / dev= 17 / gene		/codoc=_carl=_r /product==nicotinic acetylcholine receptor Dalpha6 subunit variant type II" /protef=inid="AAM13393.1" /h vref=inid="2015047"	/ LTAINSLATE OF THE STATE OF TH	FPEDDQHCEMKEGSWTYDGNQLDLYINSEDGGDLSPETTNGFWYLLAMGKKWTIVYA CCDEPVDITFFTQTRRTLYFSTNLIVEVOTISSMALLGFTLPPDSGEKLTLGVTIL LSLTVELMLYAEGNPTTRAPALGTYFNLIGTKOTMFWNASSVVLTVVLNYHHRTADIHEM PPWIKSYPLQWLPWILRMGRPGRKITRKTILLSNRMKELELKERSSKSLLANVLDIDD	Drailsasolalessasekriveeharalgenakühilikelgeitarmakadü EBELIGUWKFAAMVUDRFCLIVFTLIATVTVLLSAPHIIVQ" 793. 794 /gene"nacralpha-30D"	~ 0 Z ~ I	<pre>variation 794 /gene="nAcRalpha-30D" /note="results in glycine to serine substitution; compared to variant clone" /</pre>	/replace="a" variation 846
qa	RESULT 6 AF321446 LOCUS DEFINITION VERSION KEYWORDS	SOURCE ORGANISM REFERENCE	AUTHOI TITLE JOURNI	REPLIAND PUBMED REFERENCE AUTHORS TITLE JOURNAL	FEATURES		gene	3				Val		VAI	vai
371 AGACCAACGIGGICAGAAGGGGGGCACITGCCIGTACGIGCCACCIGGCAIATICA 430 	431 AGAGCACATGCAAGATCGACATCGCGTGGTTTCCCTTCGACGACCAACACTGTGATATGA 490		671 TCATGATAAGAAGACGTTGTACTACTTCTTCAACCTGATCGTCCGTGCGTG	1130 TCTCATCGATGGCCTACTGGGCTTCACATTGCGGCGGAGGAAACTGACGC 1189 791 TTGGAGTCACTATTCTTCTATGCTGACGGTTCCTCAACTGGTAGCCGAGACCGGG 850 1190 TGGAGTTACAATTCTTCTATCGCTGACGGTGTTCCTCAACTTGTAGCTGAGACATTGC 1249	851 CACAGGTCTCCGACGCTATCCCCCTGTTAGGGACGTACTTCAATTGCATCATGTTCATGG 910	911 TAGCSTCGTCTGTGGTACTGTGGTGCTACTCAATTACCACCATCGAACAGCTGATA 970	971 TACATGAAATGCCACAGTGGATAAAATCAGTATTCCTACAATGGTTGCCATGGATACTGC 1030 	1031 GAATGTCGAGGCAAGGAAGAAGATCACCAGGAAGACTATAATGATGAACAGGAGGATGA 1090 	1091 GGGAGCTGGAACTGAAGGGTCGTCGAGCTCCTTGCTGGCGAATGTTCTAGATATTG 1150	1151 ATGATGACTTCAGACACGGCCTCCGCTCCTAACAGTACTGCCTCGACCGGGAATTTGG 1210	1211 GACCTGGGTGCTCAATAITCCGCACGGATTTCCGTCGTCGTCCGTCCACGA 1270	1271 TGGAAGACGTGGGCGGGCTGGGTAGCCACCATGGGGGCTGCACCTCATACTGAGAG 1330	1331 AGCTGCAGTTCATCACGGCCAGGATGAAGAGGCTGATGAGGAAGCCGAGCTGATCAGCG 1390 1688 AATTGCAATTATTACGGCGGGATGCGCAAAGCTGACGAAGCGGAATGATCGCG 1747	1391 ACTGGAAGTTTGCTGCGATGGTTGTTGATAGGTTTTGCCTGTTCGTGTTCACACTTTTCA 1450	1451 CAATCATCGCGACAGTAGCTGTCCTGTTATCGGCACCGCATATCATCGTGCAA 1503

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Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology,
University College London, Gower Street, London, WC1E 6BT, UNITED
KINGDOM
 1130 TCTCATCGATGGCCCTACTGGGCTTCACATTGCCGCCGGATTCGGGCGAGAAACTGACGC
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Eukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophildae, Drosophila.
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/gene="nAcRalpha-30D"
/note="results in asparagine to serine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626 and in variant clone"
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note="compared to variant clone"
replace="t"
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Pred. No. 1.5e-188;
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/note="compared to variant
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                         /protein_id="CAD86935.1"
/baxef="101:29466435"
/tataslation="MDSPLASLSLFVLLIFLAIIXESCOGPHEKRLINHLLSTYNTLERPVANESEPLEVKFGLTLQQIIDVDEKNQLLITNLMLSLEWNDYNLRWNETEYGGYK
DALITPUKLAWRDVLAWRDDSTDFTTHTSVWFGGSCLYVPPGIEKSTCKNDIW
FPFDDQHCEMKFGSYTTDGNOLDLVLSSEDGGDLSDFITNGSWYLLAMPGKKTYTVYZ
CCPEPYVDITFTIQIRRRTLYYFFNLIVPFVLLISSMALLGFTLDPDSGEKLTLGYTTY
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PWRISVFLÇWLPWILKMGRPCRKITRKTILLSNYMKRLELEKRSSKGLLANYLDIDD
DFRHTISGGGAAIGSSASFGERPTTVEEHHTAIGCNHKDLHLILKELQFITARMRKADD
EABLIGDWKRAAWVDRFCLIVFTLFFIIATVTVLLGARHIIVQ"
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/product="nicotinic acetylcholine receptor subunit
                                                                                                                                                                                                                                                                                                                                                                                                         /product="nicotinic acetylcholine receptor subunit Dalpha6"
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 melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 747.8; DB 3;
Pred. No. 1e-187;
organism="Drosophila
             /moi_type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                            44. .121
/gene="nAcRalpha-30D"
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/gene="nAcRalpha-30D"
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Submitted (19-DEC-2003) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
reflect clone was sequenced as corracty, presence of a polyA tail and contiguity
or sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unsplaced precursor RNAS, and
reverse transcriptase errors that result in single base changes,
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu) or send email to
codna@fruitfly.berkeley.edu)

Location
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Stableton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
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/db_xref="FLYBASE:FBgn0032151"
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Pred. No. 1e-187;
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VULNYHHRTADIHEMPPWIKSVFLQWLPWILRMGRPGRKITRKTILLSNRMKELELKE RSSKSLLANVLDIDDDFRHTISGSQTAIGSSASFGRPTVEEHHTAIGCNHKDLHLIL KELQFITARMRKADDBAELIGDWKFAAMVUDRFCLIVFTLFTIATVTVLLSABHIIV Q" 836 / yene="nAcRalpha-30D" / note="results in arginine to histidine substitution;	<pre>compared to the sequence deposited in GenBank Accession Number AE003626" /replace="a" /seplace="a" /gene="nAcRalpha-30D" /one="rasults in serine to asparagine substitution; compared to the sequence deposited in GenBank Accession Number AE003626" /replace="a" / replace="a"</pre>	variation 891 //gene="nAcRalpha-30D" //gene="results in methionine to isoleucine substitution, compared to the sequence deposited in GenBank Accession //wmber AE003626" //replace="a" variation 1359 //gene="nAcRalpha-30D" //note="compared to the sequence deposited in GenBank	ation	Variation 1728 /gene="nAcRalpha-30D" /note="compared to the sequence deposited in GenBank Accession Number AE003626" /replace="c"	Query Match Best Local Similarity 68.8%; Pred. No. 5.1e-179; Length 2068; Matches 1058; Conservative 0; Mismatches 393; Indels 87; Gaps 2; Qy 11 TGTTGGCGCTTGGCGCTGCTTCCTGCCGTATCGGAGCAAGGTCCTACGAGA 70	71 71 470 131		206 TTATAACCAATATGGCTGTTGGAGTGGAATGACTACAACCTGAGGTGGAACGACA	Qy 326 TCCTTAIGEATAATAGTGCTGACGAGGTTTTGACGGGACCTACCAGACCACCACGTGG 385
QY 1271 TGGAAGACGTGGCGGCGGGTAGCCACCATCGCGAGCTGCACCTCATACTGAGAG 1330 Db 1293 TGGACGATCACACGCCATCGCAATCACAAAGATCTTCATCTAATTCTCAAAG 1352 QY 1331 AGCTGCAGTTCATCACGGCCAGGATGAAGACTCATGAGGAAGCCGAGCTGATCAGCG 1390 Db 1353 AACTGCAGTTCATCACGCCAGGATGAAGAGCTGATGAGGAAGCCCAAGCTGATCAGCG 1390	1391 1413 1451 1451	RESULT 9 AF321448 LOCUS LOCUS DEFINITION Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type IV (nAcRalpha-30D) mRNA, complete cds, alternatively spliced. ACCESSION AF321448 VERSION AF321448.1 GI:20152850	Σ		MEDLINE 21659411 PUBMED 11973307 REFERENCE 2 (bases 1 to 2068) AUTHORS Grauso,M. and Sattelle,D.B. AUTHOR Grauso,M. and Sattelle,D.B. TITLE Direct Submitssion JOURNAL Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road. Oxford Ox1	ogaster"	/cnromosone="2" /map="30D1" /dev stage="embryo" gene 12068 /gene="nAcRalpha-30D" cbs 3791907	/gene="nackalpha-300" /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3a, 3b and 8b; contains two repeats of the functional domain loop D" /codon start=1 /product="nicotinic acetylcholine receptor Dalpha6 subunit variant type IV" /protein_id="AAM13395.1" //bof_barref="ion" id="AAM13395.1" //bof_barref="ion" id="AAM13395.1" //bof_barref="ion" id="AAM13395.1" //bof_barref="ion" id="ion" id="io	/ Lanslate lon="ModelPaksis:LFVILIFIA] IKRSCQGPHEKRLINHILSTYNTI ERPVANESEDLEVKEGLTLQQI IDVDEKNQILTHAMINLDEKNQLITHINENSLEEN DYNLRWNETEYGGVKDLRITPRENGYLOLTHAMINLDEKNQLITHINTVYKRSGSCLYV PPGIFKSTCKMDITWRPFDDQHCEKKRGSWTYDGNQLDLVLNSEDGGDLSDFI TNGEW YLLAMPGKKNTIVYACCPEPYVDITFTIQIRRTLYYFFNLIYPENLIYPEVLISSMALLGFTL PPDSGEKLTLGVTILLSLTVFINLVABTLPQVSDAIPLLGTYFNCIMFWVASSVVLTV

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Variante, V. P., V. V.

Variante, V. P., V.

Ado, Xxef = 'G1: 20152883''

Ado, Xxef = 'G1: 20152883''

Ado, Xxef = 'G1: 20152883''

At anala 41: Anna-WDSPLPASLSLFVILIFLAIIXESCÇGPHEKRLINHLLSTYNTL

ERPVANESEPLEWKEGGTLLQQIIDVDEKNQILTTYNAMLLEWNDYNIRANETEYGGVK

DLRITPHKLIMKPDVLAMYNSADEGFDGTYHTNIVVKHNGSCLIVPPGGIFKSTCKMDITW

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CCPREPVYDITFTIQIRARTLYFFNILIVPCVLISSMALLGFTLAPBGSGEKLTIGVTIL

LSLTVELALVAESMFTTSDAVPLIGYTILLSLTVFINLVAETLPQVSDAIPLLGYTTY

ILLSNRAMKELELKESSKSLLAMVLDIDDDFRHTISGSGTALGSSABFGRKITRKT

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TALGCNHKDLHLIKELCRESSKSLLAMVLDIDDDFRHTISGSGTALGSSABFGRRITRKT

TALGCNHKDLHLIKELCRETTARMRKADDEAELIGDWKFAAMVUDRFCLIVFTFTII
                                                                                               2110 bp mRNA linear INV 29-APR-2002 nicotinic acetylcholine receptor Dalpha6 (nAcRalpha-30D) mRNA, complete cds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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receptor; alternatively spliced; contains exons 3a, 8a and
8b; contains two repeats of the transmembrane TM2 region"
                                                                                                                                                                                                                                                                                                  Directory and metamograter (intit 11),

Burosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 2110)

Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.

Now Putentive Nicotinic Acetylcholine Receptor Subunit Genes;

New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing

Genetics 160 (4), 1519-1533 (2002)
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/note="results in methionine to isoleucine substitution;
/comparted to the sequence deposited in GenBank Accession
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/note="compared to the sequence deposited in GenBank
Accession Number AE003626"
/replace="c"
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Grauso,M. and Sattelle,D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford (30X, UK)
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379. .1950
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/db_xref="taxon:7227"
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1. .2110
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/map="30D1"
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subunit variant type V (
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                                                                                                                                                               subunit variant type V
alternatively spliced.
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Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Noctucidea; Moduldae; Heliothinae; Heliothis.

1 (Dases 1 to 3629)
Schulle, T., Oellers, N. and Adamczewski, M.
Putative alpha subunits of insect nicotinic acetylcholine receptors
more similar to vertebrate alpha 7 subunits and C. elegans Cell
than to other insect nicotinic acetylcholine receptor alpha
                                                                                                                                                                                                                                       CGACAACGTCGGATGCTGTTCCTCTTATAGGAGTTACAATTCTTCTATCGCTCACAGTGT 1309
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Schulte, T., Oellers, N. and Adamczewski, M.
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gene="nAcRalpha-30D"
/note="compared to the sequence deposited
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/note="compared to the sequence
Accession Number AE003626"
/replace="c"
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Pred. No. 1e-162;
0; Mismatches 405;
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Nucleic acids encoding acetylcholin-receptor subunits from insects
Patent: EP 0962528-A 3 08-DEC-1999;
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Heliothis virescens
Eukaryota, Matazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endoptery/gota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
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VTILLSLTVELNMVAETMPATSDAVELLGTYFNCIMENVASSVVSTTLILNYHHRHAD
YTLLSLTVELNMVAETMPATSDAVELLGTYFNCIMENVASSVVSTTLILNYHHRHAD
IDDDFRHPQAQQPQCCRYSKGGENGATTAPPARVPPPELBLERESSKSLLANVLD
IDDDFRHPQAQQPQCCRYSKGGENGAGLAAHSCFGVDYELGLILKETRVITDQMRKD
DEDADISRDWKFAAMVUDRLCLIIFTLFTIRTIATLAVLLSAPHIMVS
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                                                                                                                                                                                                                                          /protein_id="AAD32697.1"
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/tb_xref="G1:4895005"
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YNVLERPVYNESDPFJCLSFGITLMQ1IDVDEXNQLLITNIMLKLEWNDNNLRWTSDF
GGVKDLRVPPHRLWKPDVLMYNSADEGFDSTYPTNVVVRNNGSCLYVPPGIFKSTCKI
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                       Q 18,, Leverkusen
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Pred. No. 1.1e-141;
0; Mismatches 460; Indels 40
                     Bldg.
                       AG,
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/organism="Heliothis virescens"
/mol_type="mRNA"
/db_xref="taxon:7102"
                       Bayer
Direct Submission
Submitted (19-APR-1999) ZF-BTB,
51368, Germany,
                                                          Location/Qualifiers
                                                                                                                                                     335. .1825
/note="hvnachra7-1"
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Best Local Similarity 64.6%;
Matches 929; Conservative
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Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia,
Noctuoidea; Noctuidae, Heliothinae, Heliothis.
1 (bases 1 to 3701)
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OS Heliothis virescens
BN D 200023680-A/2
BD 25-JAN-2000
PF 26-APR-1999 JP 1999118159
PR 04-MAY-1998 DE 19819829.9
PI MARTIN ADAMUTSUBUSUKI, NADJA ERASU, THOMAS SCHULTE PC
C12N15/09, AOIK67/033, CO7K14/705, CO7K16/28, C12N1/21, C12N5/10, C12Q1/68,
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Martin,A., Nadja,E. and Thomas,S.
Nucleic acid encocing insect actyl choline receptor subunit
Patent: JP 2000023680-A 2 25-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460; Indels
                                                                                                                   'note="unnamed protein product"
      organism="Heliothis virescens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                   /protein_id="CAC07500.1"
/db_xref="GI:9996845"
                              Ltype="unassigned
xref="taxon:7102"
                                                                                                                                                 codon_start=1
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64.6%;
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Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology,
University College London, Gower Street, London, WCLE 6BT, UNITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTTCACAATCATCGCGACAGTAGCTGTCCTGTTATCGGCACCGCATATCATCGTG 1500
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                                                                                                                                                 1024 ATACTGCGAATGTCGAGGCCAGGGAAGAAGATCACCAGGAAGACTATAATGATGAACACG
                                                                                                                                                                                    GCTGATATACATGAAATGCCACAGTGGATAAAATCAGTATTCCTACAATGGTTGCCATGG
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Drosophila melanogaster
Bukaryota; MetaZoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

Millar,N.S.
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/mol_type="mRNA"
/db_xref="taxon:7227"
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/db_xref="G1:29466437"
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G01N33/15, G01N33/50// (C12N1/21, C12R1:19), C12N15/00, C12N5/00
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                                                                                                                                                                                                                                                                                                                     48;
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Pred. No. 1.1e-141;
0; Mismatches 460;
                                                  Location/Qualifiers
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/organism="Heliothis virescens"
/mol_type="genomic DNA"
/db_xref="taxon:7102"
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2907 bp mRNA linear INV 29-APR-2002 nicotinic acetylcholine receptor Dalpha5 mRNA, nAcRalpha-34E-A allele, complete cds.
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Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygoi
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroides; Drosophilidae; Drosophila
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KLSLGVTILLSLTVERLIMVAETMPATSDAVPLLGKYFRVIMFWASSVVSTILVLNYH
HRNPDTHEMSEWIRVIFLYWLPCILLRMQRPGQVGYECPPPPSSSSSSASGEKKQQIQN
VELKRSKSKSKLANVLDIDDPRCVHRKCASATLHQPTYYRTWYRQGDDGSVGFVGA
GPVVJGRLHRAISHTCLTSSAEYELALILKELMUTTEQLKKEDBTSDITRDWKFAAMV
VDRLCLIIFTLPTIIATLAVLFSAPHFIVSGVG"
            ALLDNYNSLERPVVNESDPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRW
NSSEFGGVRDLRIPPHRLWKPDVLMYNSADEGFDGTYATNVVVRNNGSCLYVPPGIFK
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ACTATTCTTCTATCGCTGACGGTGTTCCTCAACCTGGTAGCCGAGACCCTGCCACAGGTC
                                                        872 ACAATTCTATTATCGCTTACAGTCTTCCTCAACATGGTGGCCGAAACAATGCCGGCGACC
                                                                                                                    TCCGACGCTATCCCCCTGTTAGGGACGTACTTCAATTGCATCATGTTCATGCTAGCGTCG
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2112 TCGAAATGCTGATACGCACGAAATGTCCGAATGGATACGCATCGTGTTTTTGTGCTGGCT
                                                                                                         Score 521.6; DB 3;
Pred. No. 1.9e-127;
0; Mismatches 519;
                                                                                                          34.7%;
61.8%;
                                                                                                                                             Conservative
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/db_xref="G1:20152840"
/db_xref="G1:20152840"
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VLQVLLVSLQQWQLHVQQRSSVLLFRRIAASTIAFISTIGSFAAQLKNSSSSSSSNSS
NNSSTQLINGLANGRAFFLITLITALIASTIAFISTIGSFAAQLKNSSSSSSSSSS
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DPLQLSFGLTLMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHR
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REMFGSWYTDOFQLDLQLOGDGTGGDISSYLNMGSWBLLGVPGRRNBITYNCCPBFYID
ITFAIIIRRYLLYYFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGYTILLSITVFLN
MVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRNADTHEMSEWIRIVE
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DDDPRHNCRPMTPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSST
EYELGLILKEIRFITDQLRKDDBCNDIANDWKFAAMVVDRLCLIIFTWFAILATIAVL
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compared to B allele"
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                                                                             Direct Submission
Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FGU,
University of Oxford, South Park Road, Oxford OX1 3QX, UK
                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="nicotinic acetylcholine receptor Dalpha5
                                                                                                                                                                                                                                                                                                                                                                 'note="ion channel; neurotransmitter transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="results in phenylalanine to isoleucine
substitution; compared to B allele"
/replace="c"
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/gene="nAcRalpha-34E"
/note="results in lysine of compared to B allele"
 Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                                                          organism="Drosophila
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. .2907
'gene="nAcRalpha-34E"
                                                                                                                                                                                        /mol_type="mRNA"
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/chromosome="2"
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Grauso, M. and Sattelle, D.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 CATTGACGTGGACGAGAAATCAACTACTTATAACCAATATATGGCTGTCGTTGGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1332 TATCGATGTGGACGAGAAAATCAATTGCTAGTCACTAATGTGGGGTGTAAACTGGAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 CACGCCCAACAAGTTGTGGAAGCCGGACGTCTTATGTATAATAGTGCTGACGAGGGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
/gene="nAcRalpha-34E"
foote="results in asparagine to serine substitution;
compared to B allele"
/replace="g"
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                                                                                                                                                                                                                                                                                                                                                   Length 2907;
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1065 2231	1106	1166 2351	1215 2411	1274	1325 2531	1385 2591	1445 2651	
GCCATGGATACTGCGAATGTCGAGGCCAQGGAAGAAGATCACCAGGAAG		GGAGAGGTCGTCGAAGTCCTTGCTGCTGGCGAATGTTCTAGATATTGATGATGATTCTAGACACACAC	CGGCCCTCCGCCTCCTAACAGTACTGCCTCGACCGGGAATTTGGGACTT	GGGTGCTCAATATTCCG-CACGGATTTCCGTCGTCGTTCGTCCGTCCGTCCGTCCACCGATGGA GGTTTATGGACAAGGCGACGATGGCAGCATTGGGCAGCAGCAGCAGGATGGGCAGATTGGCCAGCACCCGAATGCCGGA	AGACGTGGGGGGGGGGGTAGGCACCATCGCGAGCTGCACCTCATACT	GAGAGAGCTGCAGTTCATCACGGCCAGGATGAAGAAGGCTGATGAGGAAGCCGAGCTGAT 	CAGCGACTGGAAGTTTGGTGCGATGGTTGTTGATAGGTTTTGCCTGTTCGTGTTCACACT	TITCACAATCATCGGGACAGTAGCTGTCCTGTTATCGGCACGCATATCATCGT 1499
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Search completed: May 8, 2004, 02:41:32 Job time : 5963.59 secs

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GenCore version 5.1.6
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7, 2004, 10:08:00 ; Search time 604.489 Seconds (without alignments) 10562.710 Million cell updates/sec Мау 00: Run

US-09-303-232-5_COPY_95_1597 Title:

1503 Perfect score:

1 atggcccctatgttggcggc.........accgcatatcatcgtgcaa 1503 Sequence:

3373863 segs, 2124099041 residues Gapop 10.0 , Gapext 1.0 Searched:

IDENTITY NUC

Scoring table:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries N Geneseg 29Jan04:* Database

geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* geneseqn2000s:*
geneseqn2001as:* geneseqn2003bs:* geneseqn1980s:* geneseqn1990s:* geneseqn2003cs:* geneseqn2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query	Length	DB	Q	Description
1	1503	0	3109	٣	AAZ24477	Aaz24477 H. viresc
01	575.6	38.3	1540	4	ABL07231	
m	575	38.3	3700	٣	AAZ24476	
4	430.6	28.6	936	4	ABL13733	
Ŋ	411.4	27.4	2886	e	AAZ24475	
9	377.2	25.1	1509	m	AAC58395	Aac58395 Human PRO
7	374	24.9	1509	4	AAC90380	
89	374	24.9	1876	7	AAT48239	
6	374	24.9		00	ADA10864	
10	373.6	24.9	1590	7	AAV44687	
11	373.6	24.9	_	~	AAV12197	
12	373.6	24.9	1876	9	ABS54875	Abs54875 Human neu
13	373.6		1876	9	ABV73248	
14	372.4	24.8	1509	4	AAC90385	Aac90385 Mutant hu
15	372.4	24.8	1509	4	AAC90386	Aac90386 Mutant hu
16	370.8	24.7	1509	4	AAC90387	Aac90387 Mutant hu
17	363.2	24.2	1964	9	ABZ11298	
18	342.4	22.8	2769	~	AAT59196	
19	326.8	21.7	2101	7	AAT59197	Aat59197 Neuronal
20	322.8	21.5	1869	9	AAL45873	Aal45873 Modified
21	322.8	21.5	1869	9	ABL54794	Abl54794 Modified
22	304.4	20.3	2082	~	AAT59527	Aat59527 Alpha4 su
23	304.4	20.3	2752	0	ADB78668	Human n

Adb78671 Human nic Adb78670 Human nic	Adb78661 Human nic Adb78672 Human nic	Human	Human	Adb/8662 Human nic bdh/8673 Himan nic			Ada10858 Human neu	Adc71168 Human 205	Aas91552 DNA encod	Aat59528 Alpha4 su	Adb78660 Human nic	Aat48236 Neuronal	Adal0856 Human neu	Aav12199 Human neu	Aaq90387 Alpha 2 s	Abs54870 Human neu	Abv73243 Human neu	Aat48235 Neuronal
ADB78671 ADB78670	ADB78661 ADB78672	ADB78663	ADB78669	ADB/8662 ADB78673	ADE85024	AAT48237	ADA10858	ADC71168	AAS91552	AAT59528	ADB78660	AAT48236	ADA10856	AAV12199	AAQ90387	ABS54870	ABV73243	AAT48235
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20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.5	20.1	20.1	20.1	20.1	20.1	20.1	20.1	20.1	20.1	20.1
304.4	304.4	304.4	304.4	304.4	304.4	304.4	304.4	303.8	302.8	302.8	302.8	302.2	302.2	302.2	302.2	302.2	302.2	302.2
2.5 4.7 5.5	26 27		5 6	0 K	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAZ24477 standard; cDNA to mRNA; 3109 AAZ24477; RESULT 1 AAZ24477

ВР

(first entry) 17-FEB-2000 H. virescens acetyl-choline receptor DNA from clone Hva7-2.

Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds.

Heliothis virescens.

DE19819829-A1

11-NOV-1999

98DE-01019829. 04-MAY-1998;

98DE-01019829. 04-MAY-1998;

(FARB) BAYER AG.

Schulte T; Adamczewski M, Oellers N,

WPI; 2000-014207/02.

P-PSDB; AAY50816.

New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.

Claim la; Page 19-22; 26pp; German.

This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere which neurotranamission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens

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1055 ACAGCTGATATACATGAAATGCCACAGTGGATAAAATCAGTATTCCTACAATGGTTGCCA
                                                                                                                                                                                                                                                                               CGTCCACGATGGAAGACGTGGGCGGGCTGGGTAGCCACCATCGCGAGCTGCACCTC
                                                                                                                                                                                                                                                                                                                                          ACACTITICA CAATCA TCGCGACAGTAGCTGTCCTGTTATCGGCGACCGCATATCATCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGATACTGCGAATGTCGAGGCCAGGGAAGAAGATCACCAGGAAGACTATAATGATGAAC
                                               ACGAGGATGAGGGAGCTGGAACTGAAGGAGGTCGTCGAAGTCCTTGCTGGCGAATGTT
                                                                                                         CTAGATATTGATGATGACTTCAGACACGGCCCTCCGCCTCCTAACAGTACTGCCTCGACC
                                                                                                                                                                          1235 CTAGATATTGATGATGACTTCAGACACGGCCCTCCGCCTCCTAACAGTACTGCCTCGACC
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neurotransmission; plant protection agent; conductance; AChR; ds
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                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176, ABL30511), expressed DNA sequences (ABL161840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3700 BP; 893 A; 953 C; 944 G; 910 T; 0 U; 0 Other;
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Pred. No. 2.5e-149;
); Mismatches 460;
                                                                                                                                                                                                                                                                                                                                                          Schulte T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1a; Page 14-17; 26pp; German.
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64.6%;
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Best Local Similarity 64.6'
Matches 929; Conservative
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                                                                                                                                                                                                                                                                        (FARB ) BAYER
                                                                                                                                                                                             04-MAY-1998;
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                                 11-NOV-11999
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
                                   547 TCGTGGACCTACGATGGGTTTCAGTTGGACCTGCAGTTGCAGGACGAAGGTGGCGAC
                                                                                                                                                                                                                                                                                                                                                                                                               CTATCGGACTTCATAACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAAGAAC
                                                                                                                    607 ATTTCTAGCTTTATAACCAATGGCGAATGGGACTTGTTAGGTGTGCCCGGTAAACGAAAT
                                                                                                                                                         ACAATAACATACGCGTGCTGCCCCCGAGCCCTACGTGGACGTCACCTTCACCATCATGATA
                                                                                                                                                                                          AGGCGCAAAACGTTGTACTATTTTTCAATCTGATTGTGCCGTGCGTACTGATCGCCTCC
                                                                                                                                                                                                                                                                                                           ATGGCACTCCTCGCCTTCACACTGCCACCAGCTCCGGAGAGAACTCACACTTGGAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding a nicotinic acetylcholine receptor from identify potential insecticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acetyl-choline receptor; nicotinic; insect; insecticide; scree neurotransmission; plant protection agent; conductance; AChR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D. melanogaster acetyl-choline receptor DNA from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "acetyl choline receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCGACGCTATCCCCCTGTTAGGGACGTA 887
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insects, used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 GGCCTGGGACTTTTAATTATGATACCGGCTTGTGCGGCTGGACCCCATGAGAAGCGGCTA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCACGCCCTTCTGGACAACTACAAGACCTGGAGCGTCCGGTGGTCAATGAATCCGAT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 CAACTGCTTATAACGAATATTTGGCTCAAATTGGAATGGAACGATATGAATCTTCGATGG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACGACAGCGAGIAIGGCGGGGTCAAGGACCICAGGAICACGCCCCAACAAGIIGIGGAAG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTCGAGTGAGTTCGGTGTGTGCGGGATCTGCGAATTCCGCCACATCGCCTATGGAAA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGGACGTCCTTAIGTATAATAGTGCTGACGAGGTTTTGACGGGACCTACCAGACCAAC 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGTGGTCAGAAGCGGCGGCAGTTGCCTGTACGTGCCACCTGGCATATTCAAGAGCACA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIGGIGGITCGCAATAATGGGAGCTGTCTGTACGTACCGCCAGGTATATTTAAGTCAACG 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57377-ABB72072). The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATTGCAACTGGAGCTTCGGACTAACACTCCATGCAGATTATCGATGTGGACGAAAAGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 35681; 21pp + Sequence Listing; English.
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Pred. No. 2.4e-109;
0; Mismatches 274;
                                                                                                                                                                                                                                               Myers EW;
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                                                                                                              23-MAR-2001; 2001WO-US009231
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Drosophila melanogaster,
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AAC58395 standard; cDNA; 1509

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(also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1535 ACCGCCGATCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTGCGGATGAGGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1835 GGGTGTGCCCGGCAAACGTAACGAGATCTATTACAACTGCTGCCCGGAACCCTATATAGA
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                                                                                                                                                                                                                                                                                                            AGGTCCTCACGAGAAGAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCG
                                                                                                                                                                                                                                                                                                                                                  AGGATATCATGAAAAGAGACTGTTACACGATCTTTTGGATCCTTATAATACACTAGAACG
                                                                                                                                                                                                                                                                                                                                                                                        117 ACCGGTGGCCAACGAGGGAACCGCTAGAGGTCAGGTTCGGCTTGACCTTGCAGCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1415 TATCGATGTGGACGAGAAAAATCAATTGCTAGTCACTAATGTGTGGTTAAAACTGGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1475 GAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 537 AAAAGATGAGGCAGGCGGCGATCTATCGGACTTCATAACAAATGGGGAGTGGTATCTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1775 ACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGCGGAGTGGGAACTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          777 AGAGAAACTCACACTTGGAGTCACTATTCTTATCGCTGACGGTGTTCCTCAACCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2015 IGAAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGTTTCTGAATATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                 1355 TCCCGTTCTCAATGAATGGACCCGTTACAATTAAGCTTTGGTTTAACTTTAATGCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 CATTGACGTGGACGAGAAGAATCAACTACTATAACCAATATATGGCTGTCGTTGGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATGACTACAACCTGAGGTGGAACGACAGCGAGTATGGCGGGGGTCAAGGACCTCAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417 ACCTGGCATATTCAAGAGCACATGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCA
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                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                            Length 2886;
                                                                                                                                                                                      Sequence 2886 BP; 942 A; 687 C; 640 G; 617 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                            Score 411.4; DB 3;
Pred. No. 8.8e-104;
0; Mismatches 256;
                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                          27.4%;
                                                                                                                                                                                                                                                                    565; Conservative
                                                                                                                                                                                                                                                 Similarity
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PR0212 PR0290, PR0341, PR0355, PR0619, PR01013, PR091025, PR010130, PR091030, PR08148, PR09313, PR01182, PR01184, PR01884, PR01184, PR0118
                                                                                                                                                                                Human, tumour, diagnosis, neoplastic disease, neoplastic cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roy MA;
                                                                                                                                                                                                   proliferation; tumourigenesis; identification; cancer; cytostatic; noctropic; neuroprotective; antiinflammatory; immunosuppressive; immunosuppressive; immunosuppressive; immunosupmant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glad disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; eromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO polypeptides, useful in of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney AL,
                                                                                                                                     Human PRO2145 nucleotide sequence SEQ ID NO:76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thirty PRO polynucleotides encoding treatment, diagnosis and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 50; Fig 57; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US005028.
99WO-US012252.
99US-0141037P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0143048P.
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2000WO-US000219,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US000376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US028313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baker KP,
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-572270/53.
P-PSDB; AAB24088.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200053755-A2
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Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-1999;
05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-1999;
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Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 U; 0 Other;

RESULT

1412

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GTCGTCGAAGTCCTTGCTGGCGAATGTTCTAGATATTGATGATGACGTCAGACACGCCCC 1172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the coding sequence for wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7.5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The
GATCACCAGGAAGACTATAATGATGAACACGAGGATGAGGGAGCTGGAACTGAAGGAGAG
                                                            caagerececececereceaecaecaecaecaececececereceaecaecaeceaereceaeae
                                                                                                                                                                                         1113 GAGCGCCGTGGCGCCGCCGCCGCCAGCAACGGGAACCTGCTGTACATCGGCTTCCGCGG
                                                                                                                                                                                                                                                     TCCGCCTCCTAACAGTACTGCCTCGACCGGGAATTTGGGACCTGGGTGCTCAATATTCCG
                                                                                                                                                                                                                                                                                                                  1173 ceresacescenceaererererecesacecesacreresesaragreresescen--e
                                                                                                                                                                                                                                                                                                                                                                                  CACGGATTTCCGTCGGTCGTTCGTCCGTCCACGATGGAAGACGTGGGCGGCGGCGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1231 GCCTGCTCCCCCACGCACGATGAGCACCTCCTGCACGGTGGGCAACCCCCCGGAGGGGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGTAGCCACCATCGCGAGCTGCACCTCATACTGAGAGCTGCAGTTCATCACGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ACCCGGACTTGGCCAAGATCCTGGAGGGCCGCTACATTGCCAACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wild-type human alpha7 ligand gated ion channel coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; alpha7 nicotinic acetylcholine gated ion chann
5-hydroxytryptamine; 5-HT3; calcium ion conductance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1473 CCTGTTATCGGCACCGCATATCATCGTG 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cereargredecreecaacricgredad 1485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA; 1509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
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P-PSDB; AAB50012.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-2000
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of ions of
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alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells
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                                                                                    Length 1509;
                                                        Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 U; 0 Other;
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Pred. No. 1.7e-93;
0; Mismatches 635; Indels
                                                                                  Query Match
Best Local Similarity 55.1%;
Matches 809; Conservative
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ligand-gated receptor; ds.
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932

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1470 GGTGGACCGCCTGTGCCTCATGGCCTTCTCGGTCTTCACCATCATCTGCACCATCGGCAT 1529
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CCTGTTAGGGACGTACTTCAATTGCATCATGTTCATGGTAGCGTCGTCGTGGGTACTGAC
                                  945 ATTGATAGCCCAGTACTTCGCCAGCACCATGATCATCGTGGGCCTCTCGGTGGTGGTGAC
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neuronal nicotinic acetylcholine receptor; ligand-gated ion channel;
synaptic transmission; gene therapy; transgenic.
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                                                                        A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAW09025) of the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammalian cells or amphibian occytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also AAT48232-38, AAT4840-41), express recombinant nAChR subunits useful for identifying cpds. that modulate the activity of human nAChRs
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                                                                                                                                                                                                                                                        Score 374; DB 2; Length 1876;
Pred. No. 1.9e-93;
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                                       Disclosure; Page 71-73; 108pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes the V247T variant of human alpha7 nicotinic acetylcholine receptor (ndchR) subunit of the invention. Cells containing the DNA are used to express the protein and to identify modulators of alpha7 naChR activity or cytoprotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating neurodegeneration, enzyme dysfunction, affective disorders and immune neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru, psychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while monoclonal antibodies are used to detect the protein for diagnosis (in vitro or by in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR, the protein has about 100-fold greater sensitivity to cholinergic receptor agonists (nicotine or acetylcholine) and response to these agonists decays more slowly, but the wild-type inward rectification is
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           Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer; neurodegeneration; enzyme dysfunction; affective disorder; therapy; immune dysfunction; diabetic neuropathy; Alzheimer's disease;
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than drugs
subtypes
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                                                                                                                                                                                                                                                 Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA
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/product= "neuronal nicotinic acetylcholine receptor
alpha-7 subunit"
                                                                                                                                                                                                                                                                          neuronal nicotinic acetylcholine receptor; alpha-7 subunit; tissue; screening; NAChR; antibody; ds.
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GGCTTTGCTGCCCGTATCGGAGCAAGGTCCTCACGAGAAGAGACTCCTGAACGCGTTGCT
                                              114 GTCGCTCCTGCACGTGTCCCTGCAAGCCGAGTTCCAGAGGAAGCTTTACAAGGAGCTGGT
                                                                                                  GGCGAACTACAACACCCTGGAGCGACCGGTGGCCAACGAGGGGAACCGCTAGAGGTCAG
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The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic accetylcholine receptors (NAKChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human encoded by the transfected nucleic acid. This sequence represents cDNA encoding the alpha 7 subunit of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCGAACTACAACACCCTGGAGCGACCGGTGGCCAACGAGAGCGAACCGCTAGAGGTCAG
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1; Mismatches 635;
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/note= "neuronal nicotinic acetylcholine receptor"
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                                                                                                                                                                                                                                                         The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nucleotides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NACNR). The compositions and methods of the present invention, which provide a means to prepare substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NACNR alpha? subunit
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                                                                                                                                                                                                                                                                                                                                                                      11 lines to conduct calcium ions, comprising specified concentrations ions of sodium, calcium and potassium at specified pH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the coding sequence for a mutant human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytrypteamine (5-H73) chimeric ligand gated ion channel (sep AAC90382 and AAB50014). The alpha7/5-H73 chimeric ion channel can be expressed by recombinant cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the present invention, resulting in preferential calcium ion conductance by the cells. The protein encoded by this sequence has th wild-type threonine residue at position 230 substituted by a proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1509 BP; 296 A; 452 C; 429 G; 332 T; 0 U; 0 Other;
Human; alpha7 nicotinic acetylcholine gated ion channel;
5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
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Mutant human alpha7 ligand gated ion channel coding sequence #1.

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standard; cDNA; 1509

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alpha7 ligand gated ion channel

Mutant human

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                                                                                                      Human, alpha7 nicotinic acetylcholine gated ion channel; mutant;
5-bydroxytryptamine; 5-HT3; calcium ion conductance; ss.
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	453 CGCGTGGTTTCCCTTCGACGACACTGTGATATGAAGTTCGGTAGCTGGACATATGA 512 	
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3. 2,	573 AACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAGAACCACAATACATAC	
	633 GTGCTGCCCGAGCCCTACGTGGACGTCACCTTCACCATCATGATAAGAAGACGAACCTT 692 	
	693 GTACTACTTCTTCAACCTGATCGTCCGTGCGTGCTGATCTCATCGATGGCACTCCTCGG 752 	
•	753 CTTCACACTGCCACCAGACTCCGGAGAAACTCACACTTGGAGTCACTATTCTTCTATC 812	
~ ~	813 GCTGACGGTGTTCCTCAACCTGGTAGCCGAGACCCTGCCACAGGTCTCCGACGCTATCCC 872 	
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RESULT 1 BG632919/c LOCUS DEFINITION

BG632919
GH16126.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cone GH16126 3 similar to CG4128: FBan0004128 BG632919

BG632919.1 GI:13758409 ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (bases I to 885)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M. REFERENCE

BDGF/HHMI Drosophila EST Project Unpublished (2001) Other ESTS: GH16126.5prime Contact: Stapleton, M. TITLE JOURNAL DMMENT AUTHORS

Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu Based upon the presence of a XhoI site followed by a run of 14 or

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Unpublished (2001)
Other ESTs: GH15518.3prime
Contact: Stapleton, M.
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ilarity 76.7%;
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/mol_type="mRNA":727"
/clone="GH16126"
/sex="male and female"
/sex="male and female"
/dev stage="adult"
/lab_host="nDH5"
/lab_host="nDH5"
/clone_lib="GH Drosophila melanogaster head pOT2"
/nore="Organ: head; Vector: pOT2; Site_1: EcoR1; Site_2: /nore="Organism: head; Vector: pOT2; Site_1: EcoR1; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
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been removed. hit
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                                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 885;
more T residues at the beginning of the sequence, polyadenylated. The resulting Poly-T sequence has genomic AE003511: arm:X [18792641,19136447] estimated-cyto:183431866: 04/10/2001 Plate: GH.161 row: C column: 2 High quality sequence stop: 784.
                                                                                                                                                                                                                                                                                                                                                                      Score 423.8; DB 12; Length
Pred. No. 1.7e-95;
0; Mismatches 262; Indels
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68.9%;
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941 TACTCAATTACCACCATCGAACAGCTGATATACATGAAATGCCACAGTGGATAAAATCAG 1000
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GHI5518.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GHI5518 5 similar to CG4128: FBan0004128 'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence. AI292581
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//dev stage="adult"
//lab host="DH5 - alpha"
/clone lib="GH Drosophila melanogaster head pOT2"
/clone_lorgan: head, Vector: pOT2; Site_1: EcoR1; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid CDNA library."
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 607)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
                                                                                                                                                                   11 TGTTGGCGGCCTTGGCGCTGCTGCTTTGCTGCCCGTATCGGAGCAAGGTCCTCACGAGA
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
ht genomic AE003626: arm:2L [9617316, 9882551]
estimated-cytc:30C7-30F4: 04/10/2001
Plate: GH:155 row: B column: 6
High quality sequence stop: 521
POLYA=No.
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Pred. No. 3.1e-72;
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/db_xref="taxon:7227"
/clone="GH15518"
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      881
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212

495 272 332 615 675 452 735 512 795 572 632 912 692

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AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens AL530299.2 GI:31068132
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                                                                                                                                                                                                                                                              GTATAATAGTGGTGAGGGTTTTGACGGGACCTACCAGACCAACGTGGTGGTCAGAAG 392
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                                                                                                                       CAATATATGGCTGTCGTTGGAGTGGAATGACTACAACCTGAGGTGGAACGACAGCGAGTA
GTTCGGCTTGACCTTGCAGCAAATCATTGACGTGGACGAAGAATCAACTACTTATAAC
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/note="Vector: pDrive Cloning Vector: RT-PCR was performed note="Vector: pDrive Cloning Vector: RT-PCR was performed sing gene-specific primers flanking the open-reading frame. PCR products were subcloned into pDrive Cloning Vector and sequenced completely using M13 forward and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD013901 2296 bp mRNA linear EST 21-OCT-2003 90134548 Single gene library Homo sapiens CDNA, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2296)
                                                                                                                         AGAAGAATCAGCTTCTCATAACGAATCTTTGGCTTTCGTTGGAGTGGAACGACTACAATC
                                                                                                     TGAGGTGGAACGACAGCGAGTATGGCGGGGTCAAGGACCTCAGGATCACGCCCAACAAGT
                                                                                                                                                                        TGTGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTTGACGGGACCTACC
                                                                                                                                                                                                        TGTGGAAGCCCGACGTGTCATGTACAACAGCGCGGATGAGGGATTCGATGGCACGTATC
                                                                                                                                                                                                                                            AGACCAACGTGGTGGTCAGAAGCGGCGGCAGTTGCCTGTACGTGCCACCTGGCATATTCA
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 AATCGGAGCCCCTGGAGGTTAAGTTCGGACTGACGCTGCAGATGATCATCGACGTGGACG
                                  AGAAGAATCAACTTATAACCAATATATGGCTGTCGTTGGAGTGGAATGACTACAACC
                                                                                                                                                                                                                                                                         ACACCAGCGTTGTGGTCAAACATGGCGGCAGTTGTCTGTACGTGCCCCCTGGTATCTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 302.2; DB 14; Length 2296;
Pred. No. 1.2e-64;
0; Mismatches 433; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                    AGTICGGIAGCIGGACAIAIGACGCCAAICAGIIGGAICIGGIGCIAA 538
                                                                                                                                                                                                                                                                                                                                                                                                        AATTCGGTAGTTGGACTTACGATGGAAATCAGTTTGGATTTGG 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug target genes

Unpublished (2003)

Contact: Jin, P.

Incyte Corporation

Talo Porter Drive, Palo Alto, CA 94304,

Tel: 650 621 8639

Fax: 650 621 8965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Au-Young, J. and Stuve, L.L.
PCR isolation and cloning of novel spli
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/db_xref="taxon:9606"
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GSS 15-DEC-2003
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                                                                                                                                                                                                                       TGCTGATCTCATCGATGGCACTCCTCGGCTTCACACTGCCACAGACTCCGGAG--AGAA 782
                                                                                                                                                                      TCACAGTGACCATGCGCCGCAGGACGCTCTACTATGGCCTCAACCTGCTGATCCCCTGTG 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 1436) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, B., Ferriera, S., Wanghy, B., Ferriera, S., Wanghy, J., Adams, M.D. and Cargill, M. Mite, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            אומ 1436 bp DNA linear GSS 15-DEC:
Homo sapiens CHRNA3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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Location/Qualifiers
                                                                      728 CCGGCAAGAGGAGTGAAAGGTTCTATGAGTKCTGCAAAGAGCCCTACCCCGATGTCACCT
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                       CAGGCAAAAAGAACACAATAACATACGCGTGCTGCCCCGAGCCCTACGTGGACGTCACCT
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Pred. No. 7e-63;
0; Mismatches 417;
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Rockville, MD 20850, USA
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/locus_tag="HCM1369"
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSODDOO7YBO5"
/tissue type="NEUROBLASTOWA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                              On Feb 13, 2011 this sequence version replaced gi:12793792. Contact: Genoscope Genoscope - Centrar National de Sequencage Genoscope - Centrar National de Sequencage Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Amas normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7646.r. For more information about this cluster, see
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
1 (bases 1 to 201)
1 (Gruber, C., Jessee, J. and Polayes, D.
Full-length cDBA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                      cgi-bin/cluster.cgf?eeq=CSOD007CH03QP1&cluster=7646.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODD007CH03QP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    545 AGGCAGGCGCCGATCTATCGGACTTCATAACAAATGGGGAGTGGTATCTAATAGGAATGC
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Craniata, Vertebrata, Euteleostomi, Sciurognathi, Muridae, Murinae, Mus.

Chordata; Rodentia;

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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P. Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Cawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 344 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length CDNA
Meth. Enzymol. 303, 19-44 (1999)
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                                                     Mus musculus (house mouse)
                                                                                             Eukaryota; Metazoa;
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Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Icoh, M., Kagawa, T., Kasuda, T., Katoh, H., Kawai, J., Kojima, Y., Komdo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakahi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Santo, R., Saito, H., Sakai, C., Sakai, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Takahashi, F., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomatu, A., Toya, T., Yasunishi, A. The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDRAs

Nature 420, 563-573 (2002)

6 (bases I to 2940) Submitted (16-UL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. the 9 Team and Division of Experimental Animal Research in Riken contributed Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222. Fax:81-45-503-9216) The RIKEN Genome Exploration Research Group Phase II prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ Muramatsu, M. and Hayashizaki, Y. Direct Submission FANTOM Consortium.

HTC 18-SEP-2003

Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330165116 product:cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.

mRNA

2940 bp

AK034228

DEFINITION

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Sciurognathi, Muridae; Murinae; Mus
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Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone: C630019M18 product: cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.
                                                                                                                                                                             714 TGGACCAACT---GGACTTCTGGGAAAGTGGGGAGTGGGTCATTGTGGATGCCGTGGGCA
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                                                                                                                                                                                                                                                     AAAAGAACACAATAACATACGCGTGCTGCCCCGAGCCCTACGTGGACGTCACCTTCACCA
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With efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
99279253
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HTC; CAP trapper.
Mus musculus (house mouse)
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Mammalia; Eutheria;
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/protein_id="BAC28638.1"
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/db_xref="G1:263297871"
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DPGDYENVTSTRIPSELIWRPDIVLYRNADGGGFATHLTKTGVGWTPPRAIYK
DPGDYENVTSTRIPSELIWRPDIVLYRNADGGGFATHLTKTGVGWTPPRAIYK
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BEGILGDICKNGLSPAPTFCNRMDTAVETQPTCRSPSHKVPDLKTSSYBKASPCPSPG
SCHPPNSSGAPVLIKARSLSVGHVPSSQAAREGSIRCRSRSTOVCVSQDGAASLTESK
PTGSPASLKTRPSQLPVSDOTSPCKCTCKRESPVSPITYKAGGTKAPPQHLELSPAL
TRAVECVQYIADHLKAEDTDPSVKEDWKYVAMVIDRIFLMMFIIVCLLGTVGLELPPAL
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VTLCISVLLSLTVFLLLITEIIPSTSLVIPLIGBYLLFTMIFVTLSIVITVFVLNVH
                                                                                                                                                                                                                                                                                                                                                                                                                        mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="unnamed protein product; cholinergic receptor,
nicotinic, alpha polypeptide 4 (MGD|MG1:87888,
GB|NM_015730, evidence: BLASTN, 99%, match=1946)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 AGAGCACATGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCAACACTGTGATATGA
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                                                                                                                                                                                                                                                                                                                                         tissue_type="diencephalon"
|clone_lib="RIKEN full-length enriched
| dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 293.2; DB 11;
Pred. No. 2.5e-62;
0; Mismatches 453;
                                                                                                                                                                                                      /db_xref="FANTOM_DB:9330165116"
/db_xref="MG1:3398424"
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/clone="9330165116"
URL:http://fantom.gsc.riken.go.jp/
                                                                                                 organism="Mus musculus"
                                                                                                                                         /mol_type="mRNA"
/strain="C57BL/6J"
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55.9%;
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RIFSGYNKWSRPVANISDVVLVRFGILSIAQLIDVDEKNOMMTINVWVKQEWHDYKLRW
POEDDYNVTSIRIPSELIMEPDIVINNADGDFAVTHLITAMHLEYDGWYWTPATIK
SSCSIDVTFPFPDGOMCTMKFGSWYDYRAKIDLVSMHSRVDQLDFWBSGEWYIVDAVG
TYNTRKYECCAEIYPDITYAFIIRRLDFYTINLIIPCLLISCLTVLVFYLPSECGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hiori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kawai, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Santo, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Zakain, M., Tagawa, M., Tagawa, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Murata, Y., and Hayashizaki, Y., Yasunishi, A., Murata, M., Murataka, T., Toya, T., Yasunishi, A., A., Takahashi, P., Takahira, S., Murata, C., L., A., Toya, T., Yasunishi, A., A., Takahashi, A., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission

Submitted (16-APR-2002) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (SSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
URL: http://genome.gsc.riken.go.jp,
Tel:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'tissue_type="hippocampus"
'clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                on functional annotation
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               Kawai, J
                                                                                                                                                                                                 RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                            FANTOM Consortium and the RIKEN Genome Exploration Research
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cholinergic receptor, (MGD|MGI:87888,
                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nicotinic, alpha polypeptide 4 (MGD|MGI:87888,
GB|NM_015730, evidence: BLASTN, 99%, match=1946)
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                                                                                                                                                                                                                                                                                                                                                 Group Phase I & II Team.
Analysis of the mouse transcriptome based of 66,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="FANTOM_DB:C630019M18"
db_xref="MGI:2417536"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Please visit our web sice in URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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'db_xref="GI:26350297"
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RSPRTHTMPAMVRRVFLDIVPRLLEFMRRPSVVKDNCRELIESHHKMANAPRRVPEDES
BPGILGDICNQGLSPAPTFCNRMDTAVETQPTCRSPSHKVPDLKTSEVEKASPCPSPG
SCHPPNSSGAPVLIKARSLSVQHVPSSQEAAEGSIRCRSRSIQYCVSQDGAASLTESK
PTGPPNSSGAPVLIKARSLSVQHVPSSQEAAEGSIRCRSRSIQYCVSQDGAASLTESK
TRAVESQAQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLMMFIIVCLLGTVGLFLPPP
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les 453;
                                                                                                                                                                                                                                                                                                                                               Score 293.2;
Pred. No. 2.7e
0; Mismatches
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ilarity 55.9%;
Conservative
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Best Local Simil
Matches 578; (
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307 AAGTTGTGGAAGCCGGACGTCCTTATGTATAATAGTGCTGACGAGGGTTTTGACGGGACC 366 261 NNNNCTGGAAGCCNACATTGTGTTATAATAATAGTGCTGACGAGGGTTTTCAGTGGGACC 320 261 NNNNCTGGAAGCCNACATTGTGTGTGTTATGGGATTTCCAGTGGAC 320 367 TACCAGACCAACGTGGTGGTCAGAAGCGGCGGCAGTTGCTGTACGTGCCACTGGCAT 426 321 GACAAGACCATACTCAAGTACACTGGGGAGGTGACTTGGATACTCCGGCCATC 380 427 TTCAAGAGCATGCAAGATGGACATGCGTGGTTTCCTTCGACGACCACACTGTGAT 486 1 TTTAAGAGCATGCAAAATCGACGTGACTACCTTCCTTCGACGACCACACTGTGAT 486 381 TTTAAAGACCAAAATCGACGACACACACTTCATTACCAAAACTGTGAT 486	487 ATGAAGTTCGGTAGCTGGACATATGACGGCAATCAGTTGGATCTGGTGCTAAAAGATGG 546 411 ATGAAGTTCGGTTCGTGGTCCTACGATAAGCGAAATCGATCTGGTCCTGA TAGAAGTTCGGTTCTGTCTACAATAAATCGGGAAATCGATCTGGTCTTGATAAGGATGCGT 498 TCTTCCATGAACATCAATTACGAGGAGGAGTGGTTCTAATAAGAATGCCA 557 607 GGCAAAGAAACAATAACATTACGGGGGGGGGTGGGCTGATCAATCA	AKO81254 AKO81254 AKO81254 AKO81254 AKO81254 AKO81254 DIOCUS Mus musculus adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030030P04 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence. AKO81254.1 GI:26099790 HTC; CAP trapper. AKO81254.1 GI:26099790 HTC; CAP trapper. Mus musculus (house mouse) OKGANISM Mus musculus (house mouse) OKGANISM Mus musculus (house mouse) AUTHORS AUTHORS AUTHORS JOURNAL High-efficiency full-length cDNA cloning JOURNAL High-efficiency full-length cDNA cloning JOURNAL METH. Enzymol. 303, 19-44 (1999)
8 6 8 6 8 6	B & B & B & B & B & B & B & B & B & B &	RESU AKO8 DOCU DOCU VERS VERYW SOUR REFE T T T T T T T T T T T T T T T T T T T
OY 911 TAGGGTGTCTGTACTGACTGTGGTGCTAATTACCACCATGGAACAGCTGATA 970	RESULT 8 AY402874 LOCUES LOCUES AY402874 AY40287 AY40387 AY4040308 AY40341389	Query Match Best Local Similarity 55.6%; Pred. No. 7.3e-61; Matches 544; Conservative 0; Mismatches 431; Indels 3; Gaps 1; Matches 544; Conservative 0; Mismatches 431; Indels 3; Gaps 1; Qy 67 GAGAAGAGACTCCTGAACGCTTTGACATACAACACCTGGACCGCTGTGGCC 126 Db 21 GAGCACCGTCTATTGAGCGGTTTTGAACATACAATGAGTACATCATTGACGTTGGCTTGACCTTGACCTTGACCTTGACCTTGACCTGTGGCC 80 Qy 127 AACGTGAGACACCACTACTTATAACCAATTTNNNGGTGCTTGACTTGA

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158

278

338 565 398 625 458 685 518 745 578

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/note="cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891, GB|NM_009602, evidence: BLASIN, 99%, match=1498)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 GGTCAAGGACCTCAGGATCACGCCCCAACAAGTTGTGGAAGCCGGACGTCCTTATGTATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 TATGAAGAAGTCCGACTCCCTTCTAAGCACATCTGGCTCCCAGATGTGGTTCTATACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459 GTTTCCCTTCGACGACCAACACTGTGATATGAAGTTCGGTAGCTGGACATATGACGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              686 CTTCCCATTTGACCAGCAGAACTGCACCATGAAGTTCCGCTCCTGGACCTACGACCGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     519 TCAGTTGGATCTGGTGCTAAAAGATGAGGCAGGCGGCGATCTATCGGACTTCATAACAAA
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                                                                                                                                                                                                                                                                                                   Length 3483
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                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                                                                                                                           Score 281.6; DB 11;
Pred. No. 2.3e-59;
0; Mismatches 389;
                               /dev_stage="adult"
                                                                                                                                                                                                                                                                                           / Match
Local Similarity 57.7%;
les 547; Conservative
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 20499374
                                                                                                                                                                                                                                                                                                                                                      Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Fujiwake, S., Inderen, T., Rashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKBN integrated sequence analysis (RISA) system--384-format genome Res. 10 (11), 1757-1771 (2000)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3483)
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Encyclopedia Project of Genome Exploration Research Group in Ri
Genomic Sciences Center and Genome Science Laboratory in RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details
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/db_xref="MG1:2413538"
/db_xref="taxon:10090"
/clone="C030030P04"
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URL:http://fantom.gsc.riken.go.jp/
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/strain="C57BL/6J"
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FANTOM Consortium.
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/ translation="Marcsnsmallesfgllmlcsgvlgtdfeerlubesrynk
Lirpatngselvyvglmvslaqlisvhereqimtnvwltqewedyrltwkpedfbnm
KKVRLDskhtmlrdpvlynnadgmysvsfysnavvsysogstrmlpratyrsacktevk
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TVFLLLISKIVPFTSLDVPLVGKYLMFTMVLVTFSIVTSSVCVLNVHHRSPTTHTMAPW
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PASMOGLAGAFQAEPAAAGLGRSMGPCSCGLREAVDGVRFIADHMRSEDDDOSVREDW
KYVAMVIDRLFLMIFVFVCVFGTIGMFLOPLFONYTATTFLHSDHSAPSSK"
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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Drivision of Experimental Animal Research in Riken contributed to prepare mouse tissues.
URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/.
Location/Qualifiers

1. 4037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="unnamed protein product; cholinergic receptor,
nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891,
GB|NM_009602, evidence: BLASIN, 99%, match=1498)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="FANTOM DB:C530044P16"
/db_xref="MGI:2417229"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="spinal cord"
/clone_lib="RIKEN full-length
/dev_stage="12 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAC33893.1"
/db_xref="GI:26340460"
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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/clone="C530044P16"
                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="C57BL/6J"
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Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs

L Mature 420, 563-573 (2002)

E ( bases 1 to 4037)

S Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Haramoto,K., Haraka,T., Hirozane,T., Hayashida,K., Hayateu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hayashida,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katch,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kawata,M., Kojima,Y., Mumazaki,R., Murata,M., Koya,S., Kurihara,C., Mateuyama,T., Miyazaki,R., Murata,M., Ohsato,N., Okaato,M., Satto,R., Satto,R., Satto,R., Satto,R., Satto,R., Satto,R., Shibata,K., Shibata,K., Shibata,K., Shibata,K., Shibata,K., Shiragawa,A., Shiraki,T., Sagabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Murata,M., Maraka,T., Tomaru,A., Toya,T., Yasunishi,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishliy T., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yohazaki, Y., Bahikawa, T., Ozawa, K., Tamaka, T., Matsuura, S., Kawai, J., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                             AK049722

Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530044416 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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         1214 GGTCTTCCTGGAGAAGCTGCCCACCCTCCTTCCTGCAGCAGCCACG 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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Direct Submission
Submitted (16-JUJ-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
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KKVRLPSKHIWLPDVVLYNNADGMYEVSFYSNAVVSYDGSIFWLPPAIYKSACKIEVK
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VKVVFLEKLPTLLFLQQPRHRCARQRLRLRRRQREREGAGTLFFREGPAADPCTCFVN
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KYVAMVIDRLFLMIFVFVCVFGTIGMFLQPLFQNYTATTFLHSDHSAPSSK"
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Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayateu,N., Hiramoto,K., Hiracane,T.,
Hori,F., Imotani,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Mateuyama,T., Miyazaki,A., Murzata,M.,
Nakamura,M., Nishi,K., Romura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tanaka,T., Tagawa,A., Takahashi,F., Takaki-Akahira,S.,
Muramatu,M., and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="12 days embryo" anriched mouse cDNA library" 080. 1714
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                                                                                                                                                                                                                                                                                                                                                                                   Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                                                                                                            Team and the
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nicotinic, beta polypeptide 2 (neuronal) (MGD|MGI:87891,
GB|NM_009602, evidence: BLASIN, 99%, match=1498)
                                                                                                                                                                                                                                                                                                                                                  The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Fax:81-45-503-9216)
   sequencing pipeline with 384 multicapillary sequencer 3enome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                         Genome Exploration Research Group Phase
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/clone lib="RIKEN full-length
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/protein_id="BAC34749.1"
/db_xref="GI:26342174"
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/db_xref="taxon:10090"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (2002)
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6 (bases 1 to 4046)
                                                                                                                                                                                                             FANTOM Consortium.
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Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN Full-length enriched library, clone:D130070121 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
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                                                             742 TGAGATTGACCTGGTGCTCAAAAGCGATGTGGCCAGC---CTGGACGACTTCACACCTAG 798
                                                                                                                                     TGGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAGAACACAATAACATACGCGTGCTG 638
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TCAGTTGGATCTGGTGCTAAAAGATGAGGCAGGCGGCGATCTATCGGACTTCATAACAAA
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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HTC; CAP trapper.
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

IN dature 420, 563-573 (2002)

E (bases I to 1864)

S Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Hayashida, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, S., Furuno, M., Hanagaki, T., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Kadawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Sawai, C., Matsuyama, T., Miyazaki, R., Ohno, M., Ohasto, N., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sahiagawa, A., Shiraki, T., Sakai, C., Sakai, K., Shirada, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaki, Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130103E14 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, M., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Mazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKRN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                    cloning
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High efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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EEIYQDITYSLYIRRLPLFYTINLIIPCLLISFLTVLVFYLPSDCGEKVTLCISVLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /profein id="BAC35404.1"
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|RPVANVSHPVIIQFEVSMSQLVKVDEVNQIMETNLWLKQIWNDYKLKWRESDYQGVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRVPAEKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WVKAVFLNLLPRVMENTRPTSTBEDARTRNFYGAELSNLNGFSRADSKSCKEGYPCQ
DGTCGYCHHRRVKISNFSANLTRSSSSESVDAVLSLSALSPEIKEA1OSVKYTAENMK
AQNVAKEIQDDWKYVAMVIDRIFLWVPILVCILGTAGLFLQPLMARDDT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTVFLLVITETIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVLNVHYRTPTTHTMPT
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                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="eyeball"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 AGAGAAGATCTGGAAACCAGACATCGTGCTTTACAACAACGCCGATGGGGGATTTCCAAGT 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACCTACCAGACCAACGTGGTGGTCAGAAGCGGCGGCAGTTGCCTGTACGTGCCACCTGG 422
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         to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="unnamed protein product; NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT (SPTR|AALS8471, evidence: FASTY, 99.8%ID, 100%length, match=1497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCGCCGCTGTCCATGCTGATGCTGTGCTGATGCTGCTGCCAGTGGCCAGGGCCTCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATGACAAAACCAAAGCTCTACTCAAGTACACAGGAGAAGTGACTTGGATCCCTCCGGC
Division of Experimental Animal Research in Riken contributed prepare mouse tissues.
Please visit our web site for further details.
URL:http://fancome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCCCCTATGTTGGCGGCCTTGGCGCTGCTTTGCTGCCCGTATCGGAGCAAGGTCC
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Pred. No. 5.5e-58;
0; Mismatches 469; Indels
                                                                                                                                                                                                                                      /mol_type="mRNA"
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/db_xref="MG1:242528"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="0 day neonate"
94. .1593
                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                              /clone="E130103E14"
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1864
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Matches 570;
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PFDYQNCTMKFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWALIKAPGYKHEIKYNCC
EEIYQDITYSLYIRRLPLFYTINLIIPCLLISFLTVLVFYLPSDCGEKVTLCISVLLS
LTVFLLVITETIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVLNVHYRTPTTHTMPT
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DGTCGYCHHRRVKISNFSANLTRSSSSESVDAVLSLSALSPEIKEAIQSVKYIAENMK
AQNVAKEIQDDWKYVAMVIDRIFLWVFILVCILGTAGLFLQPLMARDDT"
MRVPAEKIWKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 TGATATGAAGTTCGGTAGCTGGACATATGACGGCAATCAGTTGGATCTGGTGCTAAAAGA 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATCTTTAAGAGCTCATGCAAAATCGATGTGACCTACTTCCCGTTTGACTACCAAAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                               Score 275.6; DB 11; Length
Pred. No. 6.9e-58;
0; Mismatches 469; Indels
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                                                                                                                                                                                            2898. .2903
/note="putative"
                                                                                                                                                                                                                                                                                 /note="putative"
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54.7%;
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RPVANVSHPVIIQFESSMSQLVKVDEVNQIMETNLWLKQIWNDYKLKWKPSDYQGVEF
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDMAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2916)
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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/dev_stage="12 days embryo"
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URL:http://genome.gsc.riken.go.jp/
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Location/Qualifiers
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/strain="C57BL/6J"
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Location/Qualifiers
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Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730007914 product:NEDRONAL NICOTINIC
ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1147 TCCGACCACACACACATGCCCACTTGGGTCAAGGCTGTGTTTTTGAACCTTCTCCCCAG 1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Atiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation Of 60,770 (11)-length cDNAs
Nature 420, 563-573 (2002)
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Rodentia, Sciurognathi, Muridae, Murinae; Mus.
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                                                                                         1027 GACCATCCTTCCACCTCACTGTCATCCCTTGATCGGGGAGTACCTCTTCACTAT
                                                                                                                                                                                        903 GITCAIGGIAGCGICGICTGIGGIACIGACIGIGGIACICAAITACCACCAICGAAC
GACCCTGCCACAGGTCTCCGACGCTATCCCCCTGTTAGGGACGTACTTCAATTGCATCAT
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Fris sequence was made by sequencing genomic exons and ordering them based on alignment.
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Pred. No. 9.8e-58;
0; Mismatches 401;
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/organism="Homo sapiens'
/mol type="genomic DNA"
/db_xref="taxon:9606"
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/gene="CHRNB4"
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Best Local Similarity 57.0%;
Matches 547; Conservative (
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GI:39758859

AY402876.1 GSS.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION RESULT 15 AY402876

Homo sapiens (human) Homo sapiens

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951 TGCTTCCTGCACAAGCTGCCTACCTTCCTCTTCATGAAGCGCCCTGGCCCCGACAGCAGC 1010
                                                                                                                                                        831 GGCAAGTACCTCATGTTCACCATGGTGCTGGTCACCTTCTCCATCGTCACCAGGGTCTGT 890
                         700 TICITICAACCIGATCGICCCGIGCGIGCTGATCTCATCGATGGCACTCCTCGGCTTCACA 759
                                            651 ACCATCAACCTCATCATCCCCTGGGGGCTCACCACCTTGCTGGGCCATCCTCGTCTTCTAC 710
                                                                                760 CIGCCACCAGACTCCGGAGAAACTCACACTTGGAGTCACTATTCTTCTATCGCTGACG 819
                                                                                                   820 GIGITCCICAACCIGGIAGCCGAGACCCIGCCACAGGICICCGACGCTAICCCCCIGITA 879
                                                                                                                                                                                               940 GTACTCAATTACCACCATCGAACAGCTGATATACATGAAATGCCACAGTGGATAAAATCA 999
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Search completed: May 8, 2004, 06:38:57 Job time: 4044.19 secs

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5.1.6
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2004
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using sw model OM protein - protein search, 7, 2004, 11:09:28 ; Search time 43.0968 Seconds (without alignments) 3284.615 Million cell updates/sec Мау Run on:

US-09-303-232-6 Title: Perfect score:

2640 . 1 MAFWLAALALLALLPVSEQG.......bFIIIATVAVLLSAPHIIVQ 501

Sequence:

1586107 seqs, 282547505 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A Geneseq 29Jan04:* Database

geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:* geneseqp2000s:* geneseqp2001s:* geneseqp1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRAMADIES

SUMMARIES	н	501 3 AAY50816 Aav50816 Aav50816 H. viresc	3 AAY50815 Aay50815 H.	Ω	Dro	4 ABB63683 Abb63683	2 AAW44153 Aaw44153	2 AAW09025 Aaw09025	502 3 AAB24088 Aab24088 Human PRO	4 AAB82690 Aab82690	-	ABG70492	5 ABB82435 Abb82435	7 ADA10874 Human	7 ADD47051 Human	7 ADE57310 Human	2 AAW69216 Aaw69216 V274T	502 2 AAW12368 Aaw12368 Neuronal	502 4 AAB50015 Aab50015 Mutant hu	4 AAB50016 Aab50016 D		Rat	7 Mute	6	4 AAR12824	4 PAEL2824 Adel2824 (
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Ade57314 Human Pro	Ade57318 Human Pro	Aaw09022 Neuronal	Adal0857 Human neu	Ada83810 Human CHR	Ade57312 Rat Prote	Ade57316 Rat Prote	Aab50014 Chimeric	Abg70488 Human neu		Abb61954 Drosophil	Aab50018 Mature ce	Aaw44156 Human neu	Aaw09018 Neuronal	Abg70491 Human neu		Adal0863 Human neu	Abb62727 Drosophil	Aaw44155 Human neu	Aar73966 Alpha 2 s
ADE57314	ADE57318	AAW09022	ADA10857	ADA83810	ADE57312	ADE57316	AAB50014	ABG70488	ABB82431	ABB61954	AAB50018	AAW44156	AAW09018	ABG70491	ABB82434	ADA10863	ABB62727	AAW44155	AAR73966
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989.5	989.5	989.5	989.5	982.5	977.5	977.5	962.5	946.5	946.5	943	942	940.5	933	933	933	933	933	922.5	922.5
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR. H. virescens acetyl-choline receptor protein from clone Hva7-2. AAY50816 standard; protein; 501 AA. (first entry) 17-FEB-2000 AAY50816; RESULT 1

AAY50816

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AAY5
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AAY5
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Heliothis virescens DE19819829-A1 11-NOV-1999.

98DE-01019829. 04-MAY-1998;

Adamczewski M, Oellers N, (FARB) BAYER AG.

98DE-01019829.

04-MAY-1998;

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Schulte

WPI; 2000-014207/02. N-PSDB; AAZ24477 New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.

Example 1a; Page 22-23; 26pp; German

This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens

Sequence 501 AA;

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insects, used to identify potential insecticides.
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                      Example 1a; Page 17-19; 26pp; German.
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68.7%;
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Best Local Similarity 68.7°
Matches 347; Conservative
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                                                                      MAPMLAALALLALLDVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQII
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                                                                                                                                                              GTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLK
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                                                        1 MAPMLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQII
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
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                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. virescens acetyl-choline receptor protein from clone Hva7-1
          Length 501;
                                 Indels
          Score 2640; DB 3;
Pred. No. 1.2e-267;
                                0; Mismatches
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             100.08;
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                      100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
          Query Match
Best Local Similarity 100.
Matches 501; Conservative
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N-PSDB; AAZ24476.
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directed against (1)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved insectioned; or (b) genes which encode polypeptides that are involved in isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGYQLDLQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 APMLAALALLALLPVSEQ-GPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 MEMVASSVVSTILILINYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPARV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRMRELELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRTDFRRSFVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 PSTMEDVGGGLGSH-----HRELHLILRELQFITARMKKADEEAELISDWKFAAMVVDRF
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               27;
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                                                                                                                                                                                                                                                                                                                                                          Length 496;
                                                                                                                                                                                                                                                                                                                                          Score 1803.5; DB 3; Leusen.
Pred. No. 8.2e-180;
Transper 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               53; Mismatches
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63 LQQIIDVDEKNQILTINAMLNLEWNDYNLRWNETEYGGVKDLRITPNKLWKPDVLMYNSA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                  developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.5%; Score 1570.5; DB 4; Length 498; llarity 61.1%; Pred. No. 2.4e-155; Conservative 44; Mismatches 84; Indels 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 8088; 21pp + Sequence Listing; English
DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV
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Best Local Similarity
Matches 319; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                       New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
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; Pred. No. 4.2e-159;
57; Mismatches 65;
                                                                                                                                                                                                           Schulte T;
                                                                                                                                                                                                                                                                                                                                                                  Example 1a; Page 12-14; 26pp; German.
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Best Local Similarity 60.83
Matches 319; Conservative
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                                                                                                                                                                                                           Adamczewski M,
            DE19819829-A1
                                                                                                                                                                   (FARB ) BAYER
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266
                        --ILFFQFNCAMCANLIDGPTGLHIAAĞFGRETDAĞRNYTTIINSISKPCRRVH 291
                                                                                292 ADNVGCCSSYRYTHTILKRYSLKYGPIGRTIDHYYQC-RAESTYFNCIMFMVASSVVLTV 350
                                                                                                                                                                                            SKSLLANVLDIDDDFRH-----TISGSQTAIGSS-----ASFGRPTTVEEHHTAIG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABB57737-ABB72772). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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                                                      TILLSLIVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTV
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                                                                                                                                                                   SKSLLANVLDIDDDFRHGPPPPNSTASTGNLGPGCSIFRTDFRRSFVRPSTMEDVGGGLG
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FTIMIRRRILYYFFNLIVPCVLISSMALL-
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11-JUL-2000; 2000US-00614150.
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222
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Length 311;

Score 1283; DB 4; Pred. No. 1.8e-125;

48.68;

Query Match Best Local Similarity

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                                                                                                                       140 ATNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDEA 199
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                    63
                                       79
                   4 MLAALALLALLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVD
                                20 LVYGLGLLIMIPACAAGPHEKRLHAILDNYNSLERPVVNESDPLQLSFGLTLMOIIDVD
                                                              EKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTY
                                                                        QTINVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEA
                                                                                                                                              GGDLSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVL
 Gaps
                                                                                                                                                                                                                                                                                                                                               Human, neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
brain tissue; screening; NAChR; antibody.
                                                                                                                                                                                                 Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
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30; Indels
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/label= TMD1
/note= "transmembrane domain"
262. .284
/label= TMD2
/note= "transmembrane domain"
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/label= TMD4
/note= "transmembrane domain"
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 30; Mismatches
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/label= signal
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  231; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-303024/37.
N-PSDB; AAV12197.
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                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-1994;
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                                                                                                                                                                                                                                                                                                       14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-SEP-1994.
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The present sequence represents a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta NAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agoniets or antagoniets provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with none or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells that express a variety of subtypes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
Human neuronal nicotinic acetylcholine receptor subunits and DNA - also transformed cells useful for screening cpds. which modulate activity of the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
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                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                               ; Score 1258.5; DB 2;
; Pred. No. 1.4e-122;
75; Mismatches 138;
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                                                                             Claim 7; Page 80-81; 99pp; English
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48.6%;
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Best Local Similarity 48.69
Watches 250; Conservative
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                                                                                                                                                                                                                                                                                                                                                Sequence 502 AA;
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                                                                                                                                                                                                                                                                                                                                                                   host cells
                                                                                                                                                                                                                                                                                                                                                The alpha-7 subunit (AAW09025) of the human neuronal nicotinic acetylcholine receptor (nAChR) can be expressed in transformed host cells carrying alpha-7 subunit DNA (see also AAT48239). Host cells, esp. mammalian cells or amphibian occytes, expressing the recombinant alpha-7 subunit, opt. in combination with other recombinant alpha and/or beta subunits (see also AAW09018-24, AAW09006-27), can be used to examine the function of human AChR and to identify cpds. that modulate its activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 ASVEMSAVA------PPPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   408 SIFRIDFRRSFVRPSIMEDV--GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
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neurotransmitter;
                                                                                                                                                                                                                                                                              Nucleic acids encoding nicotinic acetyl:choline receptor sub-units in screening to determine the effect of drugs on the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
Neuronal nicotinic acetylcholine receptor; nAChR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.7%; Score 1258.5; DB 2;
48.6%; Pred. No. 1.4e-122;
iive 75; Mismatches 138;
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                                                                                                                                                                                                                                                                                                                        Disclosure; Page 73-74; 108pp; English.
                                                                                                                         96WO-US009775
                                                                                                                                                     95US-00484722
                                                                                                                                                                                (SIBI-) SIBIA NEUROSCIENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                           Harpold MM
           ligand-gated receptor
                                                                                                                                                                                                                                      1997-065463/06.
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                                                                                                                                                                                                                                                  N-PSDB; AAT48239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 502 AA;
                                                                                                                         37-JUN-1996;
                                                                                                                                                     07-JUN-1995;
                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 250;
                                                                                             27-DEC-1996
                                                                                                                                                                                                           Elliott KJ,
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us-09-303-232-6.rag

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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PR0212, PR0290, PR0311, PR0355, PR0619, PR0117, PR0809, PR08104, PR01085, PR01085, PR01087, PR01081, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosupressive; immunostimulant; antianglogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epitchelial disorder; stromal disorder; bastoccelic disorder; inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotides encoding PRO polypeptides, useful in the diagnosis and prevention of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gurney AL,
461 KFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO2145 protein sequence SEQ ID NO:77.
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                                                                                                                                                                                                                       AAB24088 standard; protein; 502
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99WO-US012252.
99US-0141037P.
99US-0143048P.
99US-0145698P.
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26-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotinic acetylcholine receptor; nAChR; human; acetylcholine binding protein; AChBP; mollusc; ligand-binding protein; ligand-gated ion channel; crystal; drug design; protein co-ordinate data; schizophrenia; Alzheimer's diease; nicotine addiction; Tourette's syndrome; therapy; nootropic; neuroprotective.
                                                                                                                                                                                      126
                                                                                                                                                                                                                 129
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                                                                                                                             99
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exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108. .115
/note= "conserved ligand-binding region, residues Trp108
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                                                                                                                                                                                                     30 OVLTINIMLOMSWIDHYLOWNVSEYPGVKIVRFPDGOIMKPDILLYNSADERFDAIFHIN
                                                                                                                                                                                                                                                              408 G-----RMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW
                                                                                                                             8 LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
                                                                                                                                              10 LALAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDEKN
                                                                                                                                                                                      QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN
                                                                                                                                                                                                                                             VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
                                                                                                                                                                                                                                                                                                     LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
                                                                                                                                                                                                                                                                                                                                                              247 MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
                                                                                                                                                                                                                                                                                                                                                                                                                    SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                SVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHKQRRCSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408 SIFRIDFRRSFVRPSTMEDV--GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                    Gaps
                                                                                                  51;
                                                                      Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note...conserved ligand-binding region, and Tyr173 are essential"
                                                                                                 Indels
 polynucleotide and protein sequences given in the
                                                                      DB 3;
                                                                                   48.6%; Pred. No. 1.4e-122; ive 75; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 ELKERSSKSLLANVLDIDDDFRHGPPPNSTASTGNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 KFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                       Score 1258.5;
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                                                                       47.78;
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                                                                                               250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 ASVEMSAVA-
                                                                                   Similarity
              present invention
                                           AA;
                                           Sequence 502
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                                                                      Query Match
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The present sequence is that of the alpha subunit of human nicotinic acetylcholine receptor (nAChR). The sequence includes regions that are conserved throughout the various nAChR alpha subunits and which are essential for ligand binding. The invention relates to water-soluble ligand-binding proteins darived from molluscs, especially acetylcholine-binding proteins (AChBPs) and analogues of ligand-gated ion channels, their use for screening ligands of ligand-gated ion channels. The water-soluble ligand-binding proteins are capable of chaming multimers and are amenable to crystallization. The crystal structure of AChBP is provided, and can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated ion channels and the extracellular ligand-binding domain of ligand-gated ion channels conceptor, and comprise at least the amino acids of the AChBP care capeble of binding a ligand of a ligand-gated receptor, and comprise at least the amino acids of the AChBP caper cape of the AChBP caper of the AChBP, in the same positions as in the AChBP, and also comprising amino acids determining binding to the ligand. In the chimeric proteins, at least the sesential amino acids of at least to corresponding amino acids, and preferably entire stretches have been substituted. New drugs can be developed that estectively intervene in cheuronal signalling pathways, especially where the ligand-gated ion channel is the nAChR, and the related disorder is Tourette's syndrome, channel is the nAChR, and the related disorder is Tourette's syndrome, and channel is the nAChR, and the related disorder is Tourette's syndrome, and channel is the nAChR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
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                                                                                                                                                                                                                                                                                                                                                                Water-soluble ligand-binding proteins derived from molluscs and analogs of ligand-gated ion channels, useful in drug screening assay, where the drugs identified can be used in the treatment of Alzheimer's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
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  essential"
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48.6%; Pred. No. 1.4e-122;
iive 75; Mismatches 138;
Cys212, Cys213 and Tyr217 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 252-254; 260pp; English.
                                                                                                                                                                                                                                           (TEWE-) STICHTING TECH WETENSCHAPPEN.
                                                                                                                                                                           10-FEB-2000; 2000EP-00200443.
31-OCT-2000; 2000EP-00203810.
                                                                                                                                09-FEB-2001; 2001WO-EP001457.
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nes 250; Conservative
                                                                                                                                                                                                                                                                                                                            WPI; 2001-497071/54.
                                                                                                                                                                                                                                                                                      Sixma TK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention, resulting in preferential calcium ion conductance by the cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126
                                                           407
SVVLTVVVLLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence is wild-type human alpha? nicotinic acetylcholine
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                  367 ASVEMSAVA------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC
                                                                                                                       SIFRIDFRRSFVRPSTMEDV - - GGGLGSHHRELHLILRELQFITARMKKADEBAELISDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 LALLA-LLPVSEQGPHEKRILLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Human, alpha7 nicotinic acetylcholine gated ion channel; 5-hydroxytryptamine; 5-HT3; calcium ion conductance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.7%; Score 1258.5; DB 4
48.6%; Pred. No. 1.4e-122;
tive 75; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                               Wild-type human alpha7 ligand gated ion channel
                                                                                                                                                                                 KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
                                                                                                                                                                                                               494
                                                           ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL
                                                                                                                                                                                                    KFAACVVDRLCLMAFSVFTICTIGILMSAPNFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 61-63; 77pp; English.
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                                                                                                                                                                                                                                                                                          AAB50012 standard; protein; 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2000; 2000WO-US011862.
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Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-061524/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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contacting recombinant cells with a test compound

receptors (nNAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents the alpha 7 subunit of the human nNAChR

polypeptide

cells or

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QVLTINIWLQMSWIDHYLQWNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFDATFHIN 129
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                      VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
                                                                  LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
                                                                                 MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
                                                                                                                                                          SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
                                                                                                                                                                                SVVVIVIVIQYHHDDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRPACQHKQRRCSL
                                                                                                                                                                                                                                                   SIFRIDFRRSFVRPSIMEDV--GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                                                                                                                                                                                   G-----RMACSPIHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW
                                                                                                                                                                                                                              -----PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nicotinic acetylcholine receptor; {\tt nNAChR}; receptor; {\tt 7} subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for identifying compounds that antagonists or agonists of human neuronal nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                neuronal nicotinic acetylcholine receptor alpha 7 subunit.
                                                                                                                                                                                                       ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL----
                                                                                                                                                                                                                                                                                                KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
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92US-00938154.
93US-00028031.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       & CO INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ion flux; alpha
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30-NOV-1992;
08-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, neuronal; nicotinic acetylcholine receptor; NAChR; drug screening;
immunochemistry; NAChR alpha7 subunit; receptor.
                                                                                                                              8 LALLA-LLPVSEQGPHEKRILNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
                                                                                                                                          MALLGFTLPPDSGEKLTLGVTLLLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS
                                                                                                                                                                                                                                                                                 G-----RMACSPTHDEHLIHGGQPPGGPPGAKILEEVRYIANRFRCQDESEAVCSEW
                                                                                                                                                                 QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN
                                                                                                                                                                                                                                      LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS
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                                                                                                                                                                                                                                                                                                                     ASVEMSAVA-------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC
                                                                                                                                                                                                                                                                                                                                                                              SIFRIDFRRSFVRPSIMEDV -- GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW
                                                                                                                                                                                                   127 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
                                                                                                                 51;
                                                                                                Length 502;
                                                                                                                Indels
                                                                                              Score 1258.5; DB 5;
Pred. No. 1.4e-122;
5; Mismatches 138;
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                                                                                              47.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB82435 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human neuronal NAChR alpha7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                Conservative
                                                                                                      Similarity
                                                                             Sequence 502 AA;
                                                                                                              250;
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ADA10874 standard; protein; 502

(first entry)

06-NOV-2003

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isolated nucleic acid molecule comprising a sequence of nucleotides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nictinic acetylcholine receptor (NAChR). The compositions and methods of the present invention, which provide a means to prepare synchetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NAChR alpha? subunit
                                                                                                                                                                  Cell comprising nucleic acids encoding human alpha and beta subunits of neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LALLA-LLPVSEQGPHEKRLLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN
                                                                           Elliott KJ;
                                                                                                                                                                                                                                                                                   invention relates to a suitable host cell transfected with an
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75; Mismatches 138; Indels
                                                                           Siegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.7%; Score 1258.5; DB 5;
                                                                           Chavez-Noriega LE,
                                                                                                                                                                                                                                                Example; Page 130-131; 143pp; English
01-NOV-2000; 2000US-00703951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250; Conservative
                                     (MERI ) MERCK & CO INC
                                                                         Claeps
                                                                                                             WPI; 2002-698532/75
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                                                                                                                                 N-PSDB; ABV73248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 502 AA;
                                                                           Gillespie A,
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qq 셤 ⋩ 셤 ₽ В ò à G-----RMACSPTHDEHLIHGGOPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW 460 SIFRIDFRRSFVRPSTMEDV--GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW 465 MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306 ----PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC 407 SVVLTVVVLNYHHRTADIHEMPOWIKSVFLOWLPWILRMSRPGKKITRKTIMMNTRMREL --GPGC KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499 ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL-ASVEMSAVA-367 307 367 461 247 307

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RESULT 13 ADA10874

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New nucleic acid encoding an alpha-6 or a beta-3 subunit of a human neuronal nicotinic acetylcholine receptor (nAChR), useful for identifying compounds that modulate human neuronal nAChR activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human neuronal nicotinic acetylcholine receptor nAChR. nAChR's form ligandgated ion channels that mediate synaptic transmissions between nerve and muscle and between neurons upon interaction with the neurotransmitter acetylcholine. The nucleic acid molecule is useful for identifying compounds that modulate human neuronal nAChR. The present sequence represents the amino acid sequence of the human neuronal nicotinic acetylcholine receptor, nAChR, alpha 7 subunit #1. Note: the present sequence is the sequence encoded by the nAChR alpha 7 subunit DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD
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                                                                                               Human neuronal nicotinic acetylcholine receptor alpha 7 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 502;
                                                                                                                               lpha 7 subunit; human; neuronal nicotinic acetylcholine recep
igand-gated ion channel; synaptic transmission; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
47.7%; Score 1258.5; DB 7;
Best Local Similarity 48.6%; Pred. No. 1.4e-122;
Matches 250; Conservative 75; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 67-72; 63pp; English
                                                                                                                                                                                                                                                                                                     96US-00660451.
                                                                                                                                                                                                                                                                                                                                                                                                      Harpold MM;
                                                                                                                                                                                                                                                                                                                                                                       & CO INC
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                                                                                                                                                                  transgenic, receptor
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SVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMMNTRMREL
                                                                                                                           G-----RMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW
                                                                             ASVEMSAVA-------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC
                                                                                                         SIFRIDFRRSFVRPSTMEDV - - GGGLGSHHRELHLILRELOFITARMKKADEEAELISDW
                                                                                                                                                                                                                                                                                                                                                             Human, pain, neuronal tissue, gene therapy,
spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
                                                                                                                                                            KFAAMVVDRFCLFVFTLFTIIATVAVLLSAPHII 499
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|KFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                    367 ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL
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                                                                                                                                                                                                                                                                                                                                      Human Protein NP_000737, SEQ 1D NO 12739.
                                                                                                                                                                                                                                                       ADD47051 standard; protein; 502 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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                                                                                                                                                                                                                                                                                                           (first entry)
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BAYER AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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(FARB
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pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (CNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                        7;
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ttal nerve injury; chronic constriction injury; CCI;
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                                                                                                                                                                                                                                                                                               Length 502;
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                                                                                                                                                                                                                                                                                               DB 7;
                                                                                                                                                                                                                                                                                          47.7%; Score 1258.5; DB 7;
48.6%; Pred. No. 1.4e-122;
iive 75; Mismatches 138;
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                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 48.67
Marches 250; Conservative
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                                                                                                                                                                                                                                                   Sequence 502 AA;
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spared
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derivative or allelic variation of the nucleic acid sequence. Also derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for identifying a compound composition composition and method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more compound that endulates its activity is useful for preparing a medicament for treating modulates its activity is useful for preparing a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                       New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                    Befort K,
                                                                    14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                       14-AUG-2002; 2002WO-US025765
                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                                                                                                                    Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                   2003-268312/26
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127 VVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGGD 186 187 LSDFITNGEWYLIGMPGKKNTITYACCPEPYVDVTFTIMIRRRTLYYFFNLIVPCVLISS 246 247 MALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306 QLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYQTN 126 LALLA-LIPVSEQGPHEKRILLNALLANYNTLERPVANESEPLEVRFGLTLQQIIDVDEKN 66 51; Length 502; 47.7%; Score 1258.5; DB 7; Length 48.6%; Pred. No. 1.4e-122; cive 75; Mismatches 138; Indels Query Match Best Local Similarity 48.6⁵ Matches 250; Conservative 10 67 70 g à g ð g g ₹ à à

7;

Sequence 502 AA;

366 407 407 465 460 307 SVVLTVVVLNYHHRTADIHEMPQWIKSVFLOWLPWILRMSRPGKKITRKTIMMNTRMREL 366 307 SVVVTVIVLOYHHHDPDGGKMPKWTRVILLINWCAWFLRWKRPGEDKVRPACQHKQRRCSL 408 G-----RMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEW 367 ASVEMSAVA------PPP---ASNGNLLYIGFRGLDGVHCVPTPDSGVVC 408 SIFRIDFRRSFVRPSTMEDV--GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW 466 KFAAMVVDRFCLFVFTLFTIJATVAVLLSAPHII 499 461 KFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494 367 ELKERSSKSLLANVLDIDDDFRHGPPPPNSTASTGNL g à 셤 δ g Š

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-Q=/cgn2_1/USPTO_spool/US0933232/runat_07052004_101110_23883/app_query.fasta_1.2261
-DB=/cgn2_1/USPTO_spool/US0933232/runat_07052004_101110_23883/app_query.fasta_1.2261
-DB=/cgn2_1/USPTO_spool/US0933232/runat_07052004_101110_23883/app_query.fasta_1.2261
-UNITS-ebits -START=1 -END=-1 -MATRIX=b109um62 -TRANS=human40.cdi_LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNTR-ebits -START=1 -END=-1 -MATRIX=D=0 -THR_MINEN=0 -MAXLEN=200000000
-USTR-USD-3332_@CGN_1 1 8225_@runat_07052004_101110_23883 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGICG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1 MAPMLAALALLALLPVSEQG......LFTIIATVAVLLSAPHIIVQ 501
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_vrt:*
37: em_htg_vrt:*
38: em_htg_onum:*
40: em_htg_onum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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18	1609	٥.	2886	9	AX009610	AX009610 Sequence
19	1260	7.	2087	6	HSARA7A	sapiens
20	1258.5	47.7	1509	9	AX054567	
21	1258.5	۲,	1509	σ,	HSNACHRA7	
7 7	1258.5	۲.	1876	ن م	AR055255	AR055255 Sequence
2.5	1258.5	1.14	1876	ه د	AR071403	AR071403 Sequence
4 (1258 5	: -	1876	ρų	AK1/318/	ARI73187 Sequence
26	1258.5		1876	9	AR282833	> ~
27	1258.5	7	1876	9	AX719088	AX719088 Semience
28	1258.5	•	1876	σ	HSU62436	U62436 Human nicot
29	1258.5	7.	2088	10	AF225980	AF225980 Mus muscu
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3 6	1255.5		2106	10	RATNARAD	L31619 Rattus ratt
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/db_xref="G1:4895007"
/db_xref="G1:489500
                                                                                                                                        Heliothis virescens (tobacco budworm)
Heliothis virescens
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.

(bases 1 to 3029)
Schulte,T., Oellers,N. and Adamczewski,M.
Putantive alpha subunits of insect nicotinic acetylcholine receptors
more similar to vertebrate alpha 7 subunits and C. elegans Cell
than to other insect nicotinic acetylcholine receptor alpha
                       AF143847 and 2029 bp mRNA linear INV 27-MAY-1999 Heliothis virescens putative nicotinic acetylcholine receptor alpha
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Schulte, T., Oellers, N. and Adamczewski, M. Direct Submission
Submitted (19-APR-1999) ZF-BTB, Bayer AG, 51368, Germany
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      CGTCCACGATGGAAGAGTGGGCGGGCGGCTGGGTAGCCACCATCGCGAGCTGCACCTC
                                                                 441 IleLeuArgGluLeuGlnPheIleThrAlaArgMetLysLysAlaAspGluGluAlaGlu
                                                                                                                                                 LeulleSerAspTrpLysPheAlaAlaMetValValAspArgPheCysLeuPheValPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygi
Neoptera; Endopterygcea; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
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/note="unnamed protein product"
/codon start=1
/protein id="CAC07501.1"
/db_xref="GI:9996847"
/db_xref="REMIREMBL:CAC07501"
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/organism="Heliothis virescens"
/mol_type="unassigned DNA"
/db xref="taxon:7102"
95. .1600
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DILAIPNKLMKEPUWKYNSABEDGTYHTNIUVKHSGSCLYVPPGIFKSTCKMDITW
FPFDDQHCEMKREGSWHYYDGNQIDLYINSEDGGBLSDFITNGFWYLLANGSKTCKMDITW
CCPEPYUPITTIQIRRRTLYYFFNILVPCYLISSWALLGFTLPPDSGEKITLGVTIL
LSITVFLNIVAETIPQVSBAIPLGCFYPROINGWASSVULTVVVLNYHHRTADIHEM
PWWIKSYFLQMLPWILMRGRPGFKTTWKTILLSNRKKELEIKERSSKSLLAWYLDIDD
DFRHFISGSQTAIGSSASFGRPTYVEEHHTAIGCHKDLHLILKELQFITARMRKADD
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                                                                                                                                                                                                                                                                                                                          /gene="nAcRalpha-30D"
/note="results in asparagine to serine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
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/note="results in glycine to serine substitution; comp
to the sequence deposited in GenBank Accession Number
AE003626
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2023 bp mRNA linear INV 29-APR-2002
Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6
subunit variant type III (nAcRalpha-30D) mRNA, complete cds,
alternatively spliced.
AF321447
                                                        CGTCCACGATGGAAGACGTGGGCGGGCTGGGTAGCCACCATGGGGACTGCACCTC 1414
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Anatomy and Genetics-Functional Oxford, South Park Road, Oxford OX1
                                                                                                                                                                                                                                                               LeulleSerAspTrpLysPheAlaAlaMetValValAspArgPheCysLeuPheValPhe
                                   GlyAsnLeuGlyProGlyCysSerIlePheArgThrAspPheArgArgSerPheValArg
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Erachycera; Muscomorpha;
Pphydroidea; Drosophilidae; Drosophila.
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Grauso, M. and Sattelle, D.B.
Direct Submission
Submittes (15-NOV-2000) Human Anatomy and Genetics Unit, University of Oxford, South
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variant type III"
/protein_id="AAM13394.1"
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/organism="Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
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|. .2023
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Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Reoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

E (bases 1 to 2023)

G Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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(boxein id="AMM13193" 1"

(boxein id="MAM13193" 1")

(boxein id="MOSDLARALSLEVLIFIAIIKESCQEPHEKRILINHLLSTYNTL

(controlled in id="MOSDLARALSLEVLIFIAIIKESCQEPHEKRILINHLLSTYNTL

ERPWANESERPLEVKFGITLQQIIDVDEKNQLLITNIMLSLENNDYMLKWNETENGGVK

ERPWANESERPLEVKFGITLQQIIDVDEKNQLLITNIMLSLENNDYMLKWNETENGGVK

ERPWANESERPLEVKFGYRTDGNQLDIVLNSEDGGDLSDFITNGHWYLLANDGKKNTIVY

CCPEPYVDITFITQIRRRTLYYFFNILIVPROSINGHWASSVLICHTUNTHRYADIHEM

ESTITVELLUKARSENGERTIFYRTINFTNOTINHWASSVLICHTUNTHRYADIHEM

PHYLISGEGOTALGSSASFGRPTTVEEHHTALGCHHEDLLKERSSKGLLANVLDIDD

DERHTISGEGOTALGSSASFGRPTTVEEHHTALGCHHEDLLLIKELOFITARMRKADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serine substitution; compared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon start=1
/product="nicotinic acetylcholine receptor Dalpha6 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="nAcRalpha-30D"
/note="results in glycine to asparagine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="results in asparagine to serine substitution; compared to the sequence deposited in GenBank Accession Number AE003626 and in variant clone"
                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ
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/organism="Drosophila melanogaster"
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/note="compared to variant clone"
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to variant clone"
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/note="compared to variant
/replace="a"
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/db_xref="taxon:7227"
/chromosome="2"
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/dev_stage="embryo"
1. .2023
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Grauso, M. and Sattelle, D.B.
Direct Submission
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                                               AATTTAATCGTGCCATGTGTGCTAATCTCATCGATGGCCCTACTGGGCTTCACATTGCCG
                                                                                                                                                                                                                                                                                                       ProAspSerGlyGlutysLeuThrLeuGlyValThrIleLeuLeuSerLeuThrValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1225 CTCAACCTTGTAGCTGAGACATTGCCCCAAGTATCTGATGCAATCCCCTTGTTAGGCACC
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                        TrpTyrLeuIleGlyMetProGlyLysLysAsnThrIleThrTyrAlaCysCysProGlu
                                                                                                                                               236 AsnLeulleValProCysValLeulleSerSerMetAlaLeuLeuGlyPheThrLeuPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 ArgGluLeuHisLeuIleLeuArgGluLeuGlnPheIleThrAlaArgMetLysLysAla
                                                                                                                    ProTyrValAspValThrPheThrIleMetIleArgArgArgThrLeuTyrTyrPhePhe
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alternatively spliced.
AF321446.1 GI:20152846
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1665 bp mRNA linear INV 01-APR-2003
Drosophila melanogaster mRNA for nicotinic acetylcholine receptor
subunit Dalpha6 (nAcRalpha-30D gene).
AJ554209
AJ554209.1 GI:29466434
AJ554209.1 GI:29466434
                                                                                                                  LeuGinTrpLeuDroTrpIleLeuArgMetSerArgProGlyLysiysIleThrArgiys 355
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Direct Submission
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University College London, Gower Street, London, WCIE 6BT, UNITED KINGDOM
               TACTTCAATTGCATCATGTTCATGGTCGCCCTCGTCGGTGGTGCTGACAGTAGTGGTGCTC
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="mRNA"
/db_xref="taxon:7227"
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                       /gene="nAcRalpha-30D"
/note="compared to variant clone"
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PPWIKSVFLQMLPWILRMGPGRKITRKTILLSNRWKELELKERSSKSLLAWVLDIDD
DFRHTISGSQTALGSSASFGRPTTVEEHHTALGCNHKOLHLILKELQFITARWRKADD
EAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ"
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DLR1TPNKLWKPDVLMYNSADEGFDGTYHTSVVVKHGGSCLYVPPG1PKSTCKMD1TW
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/product="nicotinic acetylcholine receptor subunit
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Direct Submission

Submitted (19-DEC-2003) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
Sequence Clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence accuracy, presence of a polyA tail and contiguity
of sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of CDNA, clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
(http://fruitfly.berkeley.edu) or send email to
caha@fruitfly.berkeley.edu) or send email to
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/
                    Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Butorera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilae, Drosophila.
I (Bases I to 1699)
Stapleton,M., Brostetin,P., Hong,L., Agbayani,A., Carlson,J.,
Champe,M., Chavez,C., Dorsett,V., Dresnek,D., Farfan,D., Frise,E.,
George,R., Gonzalez,M., Guarin,H., Kronmiller,B., Li,P., Liao,G.,
Miranda,A., Mungall,C.J., Nunco,J., Pareleb,J., Paragas,V., Park,S.,
Patel,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Rubin,G.M.
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Gaps:
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/product="GH15518p"
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155 529 175 583 195 649 215

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235 769 255 829 275 889 295 949 315

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variant type I"
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CCPEPPYVDITFTIQIRRRILYYFFNIIVPCYLISSVALLGFTLPPDSGEKLTLGVTIL
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                                                      /codon start=1
product="nicotinic acetylcholine receptor Dalpha6 subunit
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/note="results in isoleucine to methionine substitution;
compared to variant clone"
                  /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3a and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="results in serine deletion; compared to variant
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/note="results in asparagine to glycine substitution;
compared to variant clone"
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'replace="t"
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/replace="a"
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
11973307
                                                                                                  LeuLeuAlaAsnValLeuAspIleAspAspAspPheArgHisGlyProProProAsn 395
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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/dev Btage="embryo"
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Grauso, M. and Sattelle, D.B.
Direct Submission
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Variant type IV"

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| /protein id="AAM13195.1"
| /protein id="AAM13195.1"
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PROTENKRYSTETSTGGWEDIRTPREMEKRESPULMYSABABGFDFGTYHTNIVVKRSGSCLYV
PROTEKSTCKMDITMPFERDDHJCKEKKFGSWTYDGNQLDLVLMSEDGGDLSDFTTNGEW
YLLAMPGKKNTIVYACCPEPYVDITFTIQIRRRTLYYFFNLIVEVLISSMALLGFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3a, 3b and 8b; contains two repeats of the functional domain loop D"
                                                                                                                                                                                                                                                                                                                                                    INV 29-APR-2002
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify
Mew and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                                                                                                                                                                                                               ARDALAGE DESCRIPTION SOURCE DESCRIPTION SOLVER-20 Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type IV (nAcRalpha-30D) mRNA, complete cds, alternatively spliced.
AspGluGluAlaGluLeuIleSerAspTrpLysPheAlaAlaMetValValAspArgPhe
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                                                                                                                                                  1723 GACGACGAAGCGCAATTGATCGGCGATTGGAAGTTCGCGGCAATGGTTGTGGATAGATTT
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Grauso,M. and Sattelle,D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
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Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2068)
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/mol_type="mRNA"
/db_xref="taxon:7227"
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/note="results in methionine to isoleucine substitution; compared to the sequence deposited in GenBank Accession Number AE003626"
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/ db_xref="G1:20152853"

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TAIGCNHKDLHLILKELQFITARRRKADDEAELIGDWKFAAMVUDRFCLIVFTIIT
                                                                                                                                                                                                                                                     Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type V (nAcRalpha-30D) mRNA, complete cds, alternatively spliced.
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                                                                                                          ACGCTCTTCACGATTATTGCAACGGTTACGGTGCTGCTCTCCGCTCCGCACATAATCGTG 1902
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receptor; alternatively spliced; contains exons 3a, 8a and
8b; contains two repeats of the transmembrane TM2 region"
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.

Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Novel Putative and Dalpha?, in Drosophila melanogaster Identify;

Nov and Highly Conserved Target of Adenosine Deaminase Acting on

RNA-mediaced A-to-I Pre-mRNA Editing

Genetics 160 (4), 1519-1533 (2002)
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Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OXI
                                                                                      ThrLeuPheThrIleIleAlaThrValAlaValLeuLeuSerAlaProHisIleIleVal
          LeuIleSerAspTrpLysPheAlaAlaMetValValAspArgPheCysLeuPheValPhe
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/mol_type="mRNA"
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Grauso, M. and Sattelle, D.B.
Direct Submission
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KEYWORDS SOURCE Reliothis virescens (tobacco budworm) ORGANISM Heliothis virescens (tobacco budworm) ORGANISM Heliothis virescens Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Noctucidea; Noctucidea; Heliothinae; Heliothis. I (bases 1 to 3629) AUTHORS Schule, T., Oellers, N. and Adamczewski, M. TILLE more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptors	subunits JOURNAL Unpublished REFERENCE 2 (bases 1 to 3629) AUTHORS Schulte,T., Oellers,N. and Adamczewski,M. TITLE Direct Submission JOURNAL Submitted (19-APR-1999) ZF-BTB, Bayer AG, Bldg. Q 18,, Leverkusen 51368, Germany Location/Qualifiers source 1. 3629	/organism="Heliothis virescens" /mal_type="mRNA" /db_xref="taxon:7102" 3351825 /note="hvnachra7-1" /codon start=1 /product="hutative nicotinic acetylcholine receptor alpha /protein id="AAD32697.1"	/db_xref="G1:4895005" /tranlation="MGGRARRSHLAAPAGLILLLCLIMPRGARCCYHEKELLHHLLDH YNVLERPVYNESDPLQLSFGLTLMQI IDVDEKQLLTINIWLKLEWNDMULRWTSDF GGVKDLRVPPEHLWKPDVLMYNSADEGPDSTYPTNVVVRNGSCLYVPPGI FKSTCKI DITWFPPDDQRCEMKFGSWTYDGYQLDLQLQDGGGGDISSFVTNGEWELIGVPGKRNE IYNNCCEPEYIDITITTANVIRKTLYYFRNIIVPCVLIASMALLGFTLPPDSGEKLGLG VTILLSLTVFLNMVAETWPATSDAVPLLGTYFNCIMFWASSVVSTILILNYHRHAD THEMSDWIRCVFLYMVLRWSRPGSSATTPPPARVPPPDLELRERSSKSLLANVLD IDDDREHPQAQDPQCCRYYRGGEBNGAGLAAHSCFGVDYELSLILKEIRVITDQMRKD	ORIGIN Alignment Scores: Pred. No.: 7.08e-164 Length: 3629 Score: 1803.50 Matches: 347 Percent Similarity: 79.21\$ Conservative: 53 Best Local Similarity: 68.71\$ Mismatches: 78 Query Match: 3 3.31\$ Gaps: 7	US-09-303-232-6 (1-501) x AF143846 (1-3629) QY 2 AlaProMetLeuAlaAlaLeuAlaLeuLeuBeuLeuDroValSerGluGlnGly 20	21 428 41 488	Oy 61 AspValAspGluLyaAsnGluLeuLeuIleThrAsnIleTrpLeuSerLeuGluTrpAsn 80
GGTACT roTyrv cATATG snLeuI ATTTAA		1285 287 1345 307 1405	etSer 	. 2	euGln TGCAA		Db 1903 GCAACGGTTACGGTGCTCCCGCACATAATCGTGCAA 1947 RESULT 11 AF143846 LOCUS DEFINITION Heliothis virescens putative nicotinic acetylcholine receptor alpha ACCESSION AF143846 ACCESSION AF143846 LOCUS ACCESSION AF143846 ACCESSION AF143846.1 G1:4895004

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